

SEQUENCE LISTING

<110> CHIRON SRL
MASIGNANI, Vega
ARICO, Maria Beatrice

<120> Virulence-associated Adhesins

<130> PP020667.0003

<140> PCT/IB2004/002351

<141> 2004-06-25

<150> GB0315022.4

<151> 2003-06-26

<160> 65

<170> Seqwin99, version 1.02

<210> 1

<211> 223

<212> PRT

<213> Haemophilus aegyptius

<400> 1

Met Lys Arg Asn Leu Leu Lys Gln Ser Val Ile Ala Val Leu Ile Gly
1 5 10 15

Gly Thr Thr Val Ser Asn Tyr Ala Leu Ala Gln Ala Gln Ala Gln Ala
20 25 30

Gln Val Lys Lys Asp Glu Leu Ser Glu Leu Lys Lys Gln Val Lys Glu
35 40 45

Met Asp Ala Ala Ile Asp Gly Ile Leu Asp Asp Asn Ile Ala Tyr Glu
50 55 60

Ala Glu Val Asp Ala Lys Leu Asp Gln His Ser Ala Ala Leu Gly Arg
65 70 75 80

His Thr Asn Arg Leu Asn Asn Leu Lys Thr Ile Ala Glu Lys Ala Lys
85 90 95

Gly Asp Ser Ser Glu Ala Leu Asp Lys Ile Glu Ala Leu Glu Glu Gln
100 105 110

Asn Asp Glu Phe Leu Ala Asp Ile Thr Ala Leu Glu Glu Gly Val Asp
115 120 125

Gly Leu Asp Asp Asp Ile Ala Gly Ile Gln Asp Asn Ile Ser Asp Ile
130 135 140

Glu Asp Asp Ile Asn Gln Asn Ser Ala Asp Ile Ala Thr Asn Thr Ala
145 150 155 160

Ala Ile Ala Thr His Thr Gln Arg Leu Asp Asn Leu Asp Asn Arg Val
165 170 175

Asn Asn Leu Asn Lys Asp Leu Lys Arg Gly Leu Ala Ala Gln Ala Ala
180 185 190

Leu Asn Gly Leu Phe Gln Pro Tyr Asn Val Gly Lys Leu Asn Leu Thr
Page 1

195					200					205					
Ala	Ala	Val	Gly	Gly	Tyr	Lys	Ser	Gln	Thr	Ala	Val	Ala	Val	Gly	
	210					215					220				
<210>	2														
<211>	338														
<212>	PRT														
<213>	Escherichia coli														
<400>	2														
Met	Lys	Thr	Val	Asn	Val	Ala	Leu	Leu	Ala	Leu	Ile	Ile	Ser	Ala	Thr
1				5					10					15	
Ser	Ser	Pro	Val	Val	Leu	Ala	Gly	Asp	Thr	Ile	Glu	Ala	Ala	Ala	Thr
			20					25					30		
Glu	Leu	Ser	Ala	Ile	Asn	Ser	Gly	Met	Ser	Gln	Ser	Glu	Ile	Glu	Gln
		35					40					45			
Lys	Ile	Thr	Arg	Phe	Leu	Glu	Arg	Thr	Asp	Asn	Ser	Pro	Ala	Ala	Tyr
	50					55					60				
Thr	Tyr	Leu	Thr	Glu	His	His	Tyr	Ile	Pro	Ser	Glu	Thr	Pro	Asp	Thr
65					70					75					80
Thr	Gln	Thr	Pro	Thr	Val	Gln	Thr	Asp	Pro	Asp	Ala	Gly	Gln	Lys	Thr
				85					90					95	
Val	Ala	Ala	Thr	Gly	Asp	Val	Gln	Thr	Thr	Ala	Arg	Tyr	Gln	Ser	Met
			100					105					110		
Ile	Asn	Ala	Arg	Gln	Ser	Ala	Val	Thr	Asp	Ala	Gln	Gln	Thr	Gln	Ile
		115					120					125			
Thr	Glu	Gln	Gln	Ala	Gln	Ile	Val	Ala	Thr	Gln	Lys	Thr	Leu	Ala	Ala
	130					135					140				
Thr	Gly	Asp	Thr	Gln	Asn	Thr	Ala	His	Tyr	Gln	Glu	Met	Ile	Asn	Ala
145					150					155					160
Arg	Leu	Ala	Ala	Gln	Asn	Glu	Ala	Asn	Gln	Arg	Thr	Ala	Thr	Glu	Gln
				165					170					175	
Gly	Gln	Lys	Met	Asn	Ala	Leu	Thr	Thr	Asp	Val	Ala	Val	Gln	Gln	Gln
			180					185					190		
Asn	Glu	Arg	Thr	Gln	Tyr	Asp	Lys	Gln	Met	Gln	Ser	Leu	Ala	Gln	Glu
		195					200					205			
Ser	Ala	Gln	Ala	His	Glu	Gln	Ile	Asp	Ser	Leu	Ser	Gln	Asp	Val	Thr
	210					215					220				
Gln	Thr	His	Gln	Gln	Leu	Thr	Asn	Thr	Gln	Lys	Arg	Val	Ala	Asp	Asn
225					230					235					240
Ser	Gln	Gln	Ile	Asn	Thr	Leu	Asn	Asn	His	Phe	Ser	Ser	Leu	Lys	Asn
				245					250					255	
Glu	Val	Asp	Asp	Asn	Arg	Lys	Glu	Ala	Asn	Ala	Gly	Thr	Ala	Ser	Ala
			260					265					270		
Ile	Ala	Ile	Ala	Ser	Gln	Pro	Gln	Val	Lys	Thr	Gly	Asp	Val	Met	Met
		275					280					285			

Val Ser Ala Gly Ala Gly Thr Phe Asn Gly Glu Ser Ala Val Ser Val
 290 295 300
 Gly Thr Ser Phe Asn Ala Gly Thr His Thr Val Leu Lys Ala Gly Ile
 305 310 315 320
 Ser Ala Asp Thr Gln Ser Asp Phe Gly Ala Gly Val Gly Val Gly Tyr
 325 330 335
 Ser Phe

<210> 3
 <211> 1588
 <212> PRT
 <213> Escherichia coli

<400> 3
 Met Asn Lys Ile Phe Lys Val Ile Trp Asn Pro Ala Thr Gly Asn Tyr
 1 5 10 15
 Thr Val Thr Ser Glu Thr Ala Lys Ser Arg Gly Lys Lys Ser Gly Arg
 20 25 30
 Ser Lys Leu Leu Ile Ser Ala Leu Val Ala Gly Gly Met Leu Ser Ser
 35 40 45
 Phe Gly Ala Leu Ala Asn Ala Gly Asn Asp Asn Gly Gln Gly Val Asp
 50 55 60
 Tyr Gly Ser Gly Ser Ala Gly Asp Gly Trp Val Ala Ile Gly Lys Gly
 65 70 75 80
 Ala Lys Ala Asn Thr Phe Met Asn Thr Ser Gly Ser Ser Thr Ala Val
 85 90 95
 Gly Tyr Asp Ala Ile Ala Glu Gly Gln Tyr Ser Ser Ala Ile Gly Ser
 100 105 110
 Lys Thr His Ala Ile Gly Gly Ala Ser Met Ala Phe Gly Val Ser Ala
 115 120 125
 Ile Ser Glu Gly Asp Arg Ser Ile Ala Leu Gly Ala Ser Ser Tyr Ser
 130 135 140
 Leu Gly Gln Tyr Ser Met Ala Leu Gly Arg Tyr Ser Lys Ala Leu Gly
 145 150 155 160
 Lys Leu Ser Ile Ala Met Gly Asp Ser Ser Lys Ala Glu Gly Ala Asn
 165 170 175
 Ala Ile Ala Leu Gly Asn Ala Thr Lys Ala Thr Glu Ile Met Ser Ile
 180 185 190
 Ala Leu Gly Asp Thr Ala Asn Ala Ser Lys Ala Tyr Ser Met Ala Leu
 195 200 205
 Gly Ala Ser Ser Val Ala Ser Glu Glu Asn Ala Ile Ala Ile Gly Ala
 210 215 220
 Glu Thr Glu Ala Ala Glu Asn Ala Thr Ala Ile Gly Asn Asn Ala Lys
 225 230 235 240

Ala Lys Gly Thr Asn Ser Met Ala Met Gly Phe Gly Ser Leu Ala Asp
 245 250 255
 Lys Val Asn Thr Ile Ala Leu Gly Asn Gly Ser Gln Ala Leu Ala Asp
 260 265 270
 Asn Ala Ile Ala Ile Gly Gln Gly Asn Lys Ala Asp Gly Val Asp Ala
 275 280 285
 Ile Ala Leu Gly Asn Gly Ser Gln Ser Arg Gly Leu Asn Thr Ile Ala
 290 295 300
 Leu Gly Thr Ala Ser Asn Ala Thr Gly Asp Lys Ser Leu Ala Leu Gly
 305 310 315 320
 Ser Asn Ser Ser Ala Asn Gly Ile Asn Ser Val Ala Leu Gly Ala Asp
 325 330 335
 Ser Ile Ala Asp Leu Asp Asn Thr Val Ser Val Gly Asn Ser Ser Leu
 340 345 350
 Lys Arg Lys Ile Val Asn Val Lys Asn Gly Ala Ile Lys Ser Asp Ser
 355 360 365
 Tyr Asp Ala Ile Asn Gly Ser Gln Leu Tyr Ala Ile Ser Asp Ser Val
 370 375 380
 Ala Lys Arg Leu Gly Gly Gly Ala Ala Val Asp Val Asp Asp Gly Thr
 385 390 395 400
 Val Thr Ala Pro Thr Tyr Asn Leu Lys Asn Gly Ser Lys Asn Asn Val
 405 410 415
 Gly Ala Ala Leu Ala Val Leu Asp Glu Asn Thr Leu Gln Trp Asp Gln
 420 425 430
 Thr Lys Gly Lys Tyr Ser Ala Ala His Gly Thr Ser Ser Pro Thr Ala
 435 440 445
 Ser Val Ile Thr Asp Val Ala Asp Gly Thr Ile Ser Ala Ser Ser Lys
 450 455 460
 Asp Ala Val Asn Gly Ser Gln Leu Lys Ala Thr Asn Asp Asp Val Glu
 465 470 475 480
 Ala Asn Thr Ala Asn Ile Ala Thr Asn Thr Ser Asn Ile Ala Thr Asn
 485 490 495
 Thr Ala Asn Ile Ala Thr Asn Thr Thr Asn Ile Thr Asn Leu Thr Asp
 500 505 510
 Ser Val Gly Asp Leu Gln Ala Asp Ala Leu Leu Trp Asn Glu Thr Lys
 515 520 525
 Lys Ala Phe Ser Ala Ala His Gly Gln Asp Thr Thr Ser Lys Ile Thr
 530 535 540
 Asn Val Lys Asp Ala Asp Leu Thr Ala Asp Ser Thr Asp Ala Val Asn
 545 550 555 560
 Gly Ser Gln Leu Lys Thr Thr Asn Asp Ala Val Ala Thr Asn Thr Thr
 565 570 575

Asn Ile Ala Asn Asn Thr Ser Asn Ile Ala Thr Asn Thr Thr Asn Ile
 580 585 590
 Ser Asn Leu Thr Glu Thr Val Thr Asn Leu Gly Glu Asp Ala Leu Lys
 595 600 605
 Trp Asp Lys Asp Asn Gly Val Phe Thr Ala Ala His Gly Thr Glu Thr
 610 615 620
 Thr Ser Lys Ile Thr Asn Val Lys Asp Gly Asp Leu Thr Thr Gly Ser
 625 630 635 640
 Thr Asp Ala Val Asn Gly Ser Gln Leu Lys Thr Thr Asn Asp Ala Val
 645 650 655
 Ala Thr Asn Thr Thr Asn Ile Ala Thr Asn Thr Thr Asn Ile Ser Asn
 660 665 670
 Leu Thr Glu Thr Val Thr Asn Leu Gly Glu Asp Ala Leu Lys Trp Asp
 675 680 685
 Lys Asp Asn Gly Val Phe Thr Ala Ala His Gly Asn Asn Thr Ala Ser
 690 695 700
 Lys Ile Thr Asn Ile Leu Asp Gly Thr Val Thr Ala Thr Ser Ser Asp
 705 710 715 720
 Ala Ile Asn Gly Ser Gln Leu Tyr Asp Leu Ser Ser Asn Ile Ala Thr
 725 730 735
 Tyr Phe Gly Gly Asn Ala Ser Val Asn Thr Asp Gly Val Phe Thr Gly
 740 745 750
 Pro Thr Tyr Lys Ile Gly Glu Thr Asn Tyr Tyr Asn Val Gly Asp Ala
 755 760 765
 Leu Ala Ala Ile Asn Ser Ser Phe Ser Thr Ser Leu Gly Asp Ala Leu
 770 775 780
 Leu Trp Asp Ala Thr Ala Gly Lys Phe Ser Ala Lys His Gly Thr Asn
 785 790 795 800
 Gly Asp Ala Ser Val Ile Thr Asp Val Ala Asp Gly Glu Ile Ser Asp
 805 810 815
 Ser Ser Ser Asp Ala Val Asn Gly Ser Gln Leu His Gly Val Ser Ser
 820 825 830
 Tyr Val Val Asp Ala Leu Gly Gly Gly Ala Glu Val Asn Ala Asp Gly
 835 840 845
 Thr Ile Thr Ala Pro Thr Tyr Thr Ile Ala Asn Ala Asp Tyr Asp Asn
 850 855 860
 Val Gly Asp Ala Leu Asn Ala Ile Asp Thr Thr Leu Asp Asp Ala Leu
 865 870 875 880
 Leu Trp Asp Ala Asp Ala Gly Glu Asn Gly Ala Phe Ser Ala Ala His
 885 890 895
 Gly Lys Asp Lys Thr Ala Ser Val Ile Thr Asn Val Ala Asn Gly Ala
 900 905 910

Ile Ser Ala Ala Ser Ser Asp Ala Ile Asn Gly Ser Gln Leu Tyr Thr
 915 920 925
 Thr Asn Lys Tyr Ile Ala Asp Ala Leu Gly Gly Asp Ala Glu Val Asn
 930 935 940
 Ala Asp Gly Thr Ile Thr Ala Pro Thr Tyr Thr Ile Ala Asn Ala Glu
 945 950 955 960
 Tyr Asn Asn Val Gly Asp Ala Leu Asp Ala Leu Asp Asp Asn Ala Leu
 965 970 975
 Leu Trp Asp Glu Thr Ala Asn Gly Gly Ala Gly Ala Tyr Asn Ala Ser
 980 985 990
 His Asp Gly Lys Ala Ser Ile Ile Thr Asn Val Ala Asn Gly Ser Ile
 995 1000 1005
 Ser Glu Asp Ser Thr Asp Ala Val Asn Gly Ser Gln Leu Asn Ala Thr
 1010 1015 1020
 Asn Met Met Ile Glu Gln Asn Thr Gln Ile Ile Asn Gln Leu Ala Gly
 1025 1030 1035 1040
 Asn Thr Asp Ala Thr Tyr Ile Gln Glu Asn Gly Ala Gly Ile Asn Tyr
 1045 1050 1055
 Val Arg Thr Asn Asp Asp Gly Leu Ala Phe Asn Asp Ala Ser Ala Gln
 1060 1065 1070
 Gly Val Gly Ala Thr Ala Ile Gly Tyr Asn Ser Val Ala Lys Gly Asp
 1075 1080 1085
 Ser Ser Val Ala Ile Gly Gln Gly Ser Tyr Ser Asp Val Asp Thr Gly
 1090 1095 1100
 Ile Ala Leu Gly Ser Ser Ser Val Ser Ser Arg Val Ile Ala Lys Gly
 1105 1110 1115 1120
 Ser Arg Asp Thr Ser Ile Thr Glu Asn Gly Val Val Ile Gly Tyr Asp
 1125 1130 1135
 Thr Thr Asp Gly Glu Leu Leu Gly Ala Leu Ser Ile Gly Asp Asp Gly
 1140 1145 1150
 Lys Tyr Arg Gln Ile Ile Asn Val Ala Asp Gly Ser Glu Ala His Asp
 1155 1160 1165
 Ala Val Thr Val Arg Gln Leu Gln Asn Ala Ile Gly Ala Val Ala Thr
 1170 1175 1180
 Thr Pro Thr Lys Tyr Phe His Ala Asn Ser Thr Glu Glu Asp Ser Leu
 1185 1190 1195 1200
 Ala Val Gly Thr Asp Ser Leu Ala Met Gly Ala Lys Thr Ile Val Asn
 1205 1210 1215
 Gly Asp Lys Gly Ile Gly Ile Gly Tyr Gly Ala Tyr Val Asp Ala Asn
 1220 1225 1230
 Ala Leu Asn Gly Ile Ala Ile Gly Ser Asn Ala Gln Val Ile His Val
 1235 1240 1245
 Asn Ser Ile Ala Ile Gly Asn Gly Ser Thr Thr Thr Arg Gly Ala Gln

1250	1255	1260
Thr Asn Tyr Thr Ala Tyr Asn Met Asp Ala Pro Gln Asn Ser Val Gly 1265 1270 1275 1280		
Glu Phe Ser Val Gly Ser Ala Asp Gly Gln Arg Gln Ile Thr Asn Val 1285 1290 1295		
Ala Ala Gly Ser Ala Asp Thr Asp Ala Val Asn Val Gly Gln Leu Lys 1300 1305 1310		
Val Thr Asp Ala Gln Val Ser Gln Asn Thr Gln Ser Ile Thr Asn Leu 1315 1320 1325		
Asp Asn Arg Val Thr Asn Leu Asp Ser Arg Val Thr Asn Ile Glu Asn 1330 1335 1340		
Gly Ile Gly Asp Ile Val Thr Thr Gly Ser Thr Lys Tyr Phe Lys Thr 1345 1350 1355 1360		
Asn Thr Asp Gly Val Asp Ala Ser Ala Gln Gly Lys Asp Ser Val Ala 1365 1370 1375		
Ile Gly Ser Gly Ser Ile Ala Ala Ala Asp Asn Ser Val Ala Leu Gly 1380 1385 1390		
Thr Gly Ser Val Ala Thr Glu Glu Asn Thr Ile Ser Val Gly Ser Ser 1395 1400 1405		
Thr Asn Gln Arg Arg Ile Thr Asn Val Ala Ala Gly Lys Asn Ala Thr 1410 1415 1420		
Asp Ala Val Asn Val Ala Gln Leu Lys Ser Ser Glu Ala Gly Gly Val 1425 1430 1435 1440		
Arg Tyr Asp Thr Lys Ala Asp Gly Ser Ile Asp Tyr Ser Asn Ile Thr 1445 1450 1455		
Leu Gly Gly Gly Asn Gly Gly Thr Thr Arg Ile Ser Asn Val Ser Ala 1460 1465 1470		
Gly Val Asn Asn Asn Asp Val Val Asn Tyr Ala Gln Leu Lys Gln Ser 1475 1480 1485		
Val Gln Glu Thr Lys Gln Tyr Thr Asp Gln Arg Met Val Glu Met Asp 1490 1495 1500		
Asn Lys Leu Ser Lys Thr Glu Ser Lys Leu Ser Gly Gly Ile Ala Ser 1505 1510 1515 1520		
Ala Met Ala Met Thr Gly Leu Pro Gln Ala Tyr Thr Pro Gly Ala Ser 1525 1530 1535		
Met Ala Ser Ile Gly Gly Gly Thr Tyr Asn Gly Glu Ser Ala Val Ala 1540 1545 1550		
Leu Gly Val Ser Met Val Ser Ala Asn Gly Arg Trp Val Tyr Lys Leu 1555 1560 1565		
Gln Gly Ser Thr Asn Ser Gln Gly Glu Tyr Ser Ala Ala Leu Gly Ala 1570 1575 1580		
Gly Ile Gln Trp		

1585

<210> 4
<211> 295
<212> PRT
<213> Actinobacillus actinomycetemcomitans

<400> 4
Met Thr Tyr Gln Leu Phe Lys His His Leu Val Ala Leu Met Val Thr
1 5 10 15
Gly Ala Ile Ser Val Asn Ala Leu Ala Lys Asp Ser Phe Leu Glu Asn
20 25 30
Pro Ser Ala Asn Leu Pro Gln Gln Val Phe Lys Asn Arg Val Asp Ile
35 40 45
Phe Asn Asn Glu Thr Asn Ile Asn Glu Asn Lys Lys Asp Ile Ala Ile
50 55 60
Asn Lys Ala Asn Ile Ala Ser Ile Glu Lys Asp Val Met Arg Asn Thr
65 70 75 80
Gly Gly Ile Asp Arg Leu Ala Lys Gln Glu Leu Val Asn Arg Ala Arg
85 90 95
Ile Thr Lys Asn Glu Leu Asp Ile Arg Lys Asn Thr Lys Ser Ile Ala
100 105 110
Glu Asn Thr Ala Ser Ile Ala Arg Ile Asp Gly Asn Leu Glu Gly Val
115 120 125
Asn Arg Val Leu Gln Asn Val Asp Val Arg Ser Thr Glu Asn Ala Ala
130 135 140
Arg Ser Arg Ala Asn Glu Gln Lys Ile Ala Glu Asn Lys Lys Ala Ile
145 150 155 160
Glu Asn Lys Ala Asp Lys Ala Asp Val Glu Lys Asn Arg Ala Asp Ile
165 170 175
Ala Ala Asn Ser Arg Ala Ile Ala Thr Phe Arg Ser Ser Ser Gln Asn
180 185 190
Ile Ala Ala Leu Thr Thr Lys Val Asp Arg Asn Thr Ala Arg Ile Asp
195 200 205
Arg Leu Asp Ser Arg Val Asn Glu Leu Asp Lys Glu Val Lys Asn Gly
210 215 220
Leu Ala Ser Gln Ala Ala Leu Ser Gly Leu Phe Gln Pro Tyr Asn Val
225 230 235 240
Gly Ser Leu Asn Leu Ser Ala Ala Val Gly Gly Tyr Lys Ser Lys Thr
245 250 255
Ala Leu Ala Val Gly Ser Gly Tyr Arg Phe Asn Gln Asn Val Ala Ala
260 265 270
Lys Ala Gly Val Ala Val Ser Thr Asn Gly Gly Ser Ala Thr Tyr Asn
275 280 285
Val Gly Leu Asn Phe Glu Trp
290 295

<210> 5
 <211> 452
 <212> PRT
 <213> Haemophilus somnus

<400> 5
 Met Lys Lys Val Gln Phe Phe Lys Tyr Ser Ser Leu Ala Leu Ala Leu
 1 5 10 15
 Gly Leu Gly Val Ser Ala Ser Ala Leu Ala Ala Pro Thr Ser Thr Ser
 20 25 30
 Thr Thr Thr Gly Pro Glu Ala Pro Pro Thr Gly Pro Ala Pro Thr Ala
 35 40 45
 Lys Asp Pro Leu Ala Glu Thr Ala Leu Ala Tyr Asp Leu Glu Asn Glu
 50 55 60
 Val Ala Tyr Leu Arg Met Lys Ala Gly Glu Trp Met Gln Leu Gly Leu
 65 70 75 80
 Asp Pro Glu Lys Glu Val Ile Lys Gly Trp Asn Glu Val Lys Ser Leu
 85 90 95
 Pro Arg Ile Asp Gly Asn Gly Lys Asp Lys Gln Thr Lys Asp Gln Ile
 100 105 110
 Ala Met Leu Ile Arg Thr Val Asp Asn Thr Lys Glu Leu Gly Arg Ile
 115 120 125
 Val Ser Thr Asn Ile Glu Asp Ile Lys Asn Leu Lys Lys Glu Leu Tyr
 130 135 140
 Gly Phe Val Glu Asp Val Asn Glu Ser Glu Ala Arg Asn Ile Ser Arg
 145 150 155 160
 Ile Asp Glu Asn Glu Lys Asp Ile Lys Asn Leu Lys Lys Glu Leu Tyr
 165 170 175
 Asp Phe Val Glu Asp Val Asn Glu Ser Glu Ala Arg Asn Ile Ser Arg
 180 185 190
 Ile Asp Glu Asn Glu Lys Asp Ile Asn Thr Leu Lys Glu Leu Met Asp
 195 200 205
 Glu Asp Leu Asn Ser Val Leu Thr Gln Ile Glu Asp Val Lys Leu Thr
 210 215 220
 Phe Gln Asp Val Asn Asp Asn Val Asn Leu Ala Phe Glu Glu Ile Asn
 225 230 235 240
 Gly Asn Ala Gln Lys Phe Asp Thr Ala Ile Glu Gly Leu Thr Ser Gly
 245 250 255
 Leu Ser Asp Leu Gln Ala Lys Val Asp Ala Asn Lys Gln Glu Thr Glu
 260 265 270
 Asp Asp Ile Ala Asp Asn Ala Lys Ala Ile His Ser Asn Thr Lys Gly
 275 280 285
 Ile Ala Lys Asn Thr Lys Asp Ile Arg Asp Leu Asp Thr Lys Thr Lys
 290 295 300

Gln Met Leu Glu Asn Asp Lys Asn Leu Met Thr Gly Leu Glu Ser Leu
 305 310 315 320
 Ala Thr Glu Thr Ser Lys Gly Phe Glu Arg Phe Asp Val Lys Thr Gln
 325 330 335
 Gln Leu Asp Gln Ala Val Ala Asn Val Val Gly Arg Val Asp Ile Thr
 340 345 350
 Glu Gln Ala Ile Arg Gln Asn Thr Ala Gly Leu Val Asn Val Asn Lys
 355 360 365
 Arg Val Asp Thr Leu Asp Lys Asn Thr Lys Ala Gly Ile Ala Ser Ala
 370 375 380
 Val Ala Leu Gly Met Leu Pro Gln Ser Thr Ala Pro Gly Lys Ser Leu
 385 390 395 400
 Val Ser Leu Gly Val Gly His His Arg Gly Gln Ser Ala Thr Ala Ile
 405 410 415
 Gly Val Ser Ser Met Ser Ser Asn Gly Lys Trp Val Val Lys Gly Gly
 420 425 430
 Met Ser Tyr Asp Thr Gln Arg His Ala Thr Phe Gly Gly Ser Val Gly
 435 440 445
 Phe Phe Phe Asn
 450

<210> 6
 <211> 273
 <212> PRT
 <213> Haemophilus ducreyi

<400> 6
 Met Lys Ile Lys Cys Leu Val Ala Val Val Gly Leu Ala Cys Ser Thr
 1 5 10 15
 Ile Thr Thr Met Ala Gln Gln Pro Pro Lys Phe Ala Gly Val Ser Ser
 20 25 30
 Leu Tyr Ser Tyr Glu Tyr Asp Tyr Gly Lys Gly Lys Trp Thr Trp Ser
 35 40 45
 Asn Glu Gly Gly Phe Asp Ile Lys Val Pro Gly Ile Lys Met Lys Pro
 50 55 60
 Lys Glu Trp Ile Ser Lys Gln Ala Thr Tyr Leu Glu Leu Gln His Tyr
 65 70 75 80
 Met Pro Tyr Thr Pro Val Leu Val Thr Ser Ala Pro Asp Val Ser Pro
 85 90 95
 Ser Ser Ile Ser Ile Leu Leu Tyr Pro Met Ser Asp Pro Asp Gln Leu
 100 105 110
 Gly Ile Asn Arg Gln Gln Leu Lys Leu Asn Leu Tyr Ser Tyr Phe Asn
 115 120 125
 Asp Leu Arg His Asp Phe Lys Leu Lys Val Leu Asp Ala Arg Ile Ser
 130 135 140

Lys Asn Lys Gln Asn Ile Asp Thr Ile Ser Lys Tyr Leu Leu Glu Leu
 145 150 155 160
 Gly Thr Tyr Leu Asp Gly Ser Tyr Arg Met Met Glu Gln Asn Thr His
 165 170 175
 Asn Ile Asn Lys Asn Thr His Asn Ile Asn Lys Asn Thr His Asn Ile
 180 185 190
 Asn Lys Leu Ser Lys Glu Leu Gln Thr Gly Leu Ala Asn Gln Ser Ala
 195 200 205
 Leu Ser Met Leu Val Gln Pro Asn Gly Val Gly Lys Thr Ser Val Ser
 210 215 220
 Ala Ala Val Gly Gly Tyr Arg Asp Lys Thr Ala Leu Ala Ile Gly Val
 225 230 235 240
 Gly Ser Arg Ile Thr Asp Arg Phe Thr Ala Lys Ala Gly Val Ala Phe
 245 250 255
 Asn Thr Tyr Asn Gly Gly Met Ser Tyr Gly Ala Ser Val Gly Tyr Glu
 260 265 270

Phe

<210> 7
 <211> 338
 <212> PRT
 <213> Escherichia coli

<400> 7
 Met Lys Thr Val Asn Val Ala Leu Leu Ala Leu Ile Ile Ser Ala Thr
 1 5 10 15
 Ser Ser Pro Phe Val Leu Ala Gly Asp Thr Ile Glu Ala Ala Ala Thr
 20 25 30
 Glu Leu Ser Ala Ile Asn Ser Gly Met Ser Gln Ser Glu Ile Glu Gln
 35 40 45
 Lys Ile Thr Arg Phe Leu Glu Arg Thr Asp Asn Ser Pro Ala Ala Tyr
 50 55 60
 Thr Tyr Leu Thr Glu His His Tyr Ile Pro Ser Glu Thr Pro Asp Thr
 65 70 75 80
 Thr Gln Thr Pro Pro Val Gln Thr Asp Pro Asp Ala Gly Gln Lys Thr
 85 90 95
 Val Ala Ala Thr Gly Asp Val Gln Thr Thr Ala Arg Tyr Gln Ser Met
 100 105 110
 Ile Asn Ala Arg Gln Ser Thr Val Thr Asp Ala Gln Gln Thr Gln Ile
 115 120 125
 Thr Glu Gln Gln Ala Gln Ile Val Ala Thr Gln Lys Thr Leu Ala Ala
 130 135 140
 Thr Gly Asp Thr Gln Asn Thr Ala His Tyr Gln Glu Met Ile Asn Ala
 145 150 155 160

Arg Leu Ala Ala Gln Asn Glu Ala Asn Gln Arg Thr Thr Thr Glu Gln
 165 170 175
 Gly Gln Lys Met Asn Ala Leu Thr Thr Asp Val Ala Ala Gln Gln Gln
 180 185 190
 Lys Glu Arg Ala Gln Tyr Asp Lys Gln Met Gln Ser Leu Ala Gln Lys
 195 200 205
 Ser Val Gln Ala His Glu Gln Ile Glu Ser Leu Arg Gln Asp Ser Ala
 210 215 220
 Gln Thr Gln Gln Gln Leu Thr Asn Thr Gln Lys Arg Val Ala Asp Asn
 225 230 235 240
 Ser Gln Gln Ile Asn Thr Leu Asn Asn His Phe Ser Ser Leu Lys Asn
 245 250 255
 Glu Val Glu Asp Asn Arg Lys Glu Ala Asn Ala Gly Thr Ala Ser Ala
 260 265 270
 Ile Ala Ile Ala Ser Gln Pro Gln Val Lys Thr Gly Asp Leu Met Met
 275 280 285
 Val Ser Ala Gly Ala Gly Thr Phe Asn Gly Glu Ser Ala Val Ser Val
 290 295 300
 Gly Thr Ser Phe Asn Ala Gly Thr His Thr Val Leu Lys Ala Gly Ile
 305 310 315 320
 Ser Ala Asp Thr Gln Ser Asp Phe Gly Ala Gly Val Gly Val Gly Tyr
 325 330 335

Ser Phe

<210> 8
 <211> 717
 <212> PRT
 <213> Escherichia coli

<400> 8
 Met Lys Thr Val Lys Leu Ser Leu Leu Ala Val Val Val Ala Thr Ala
 1 5 10 15
 Val Ser Pro Ser Ala Phe Ala Gly Asp Thr Val Glu Ala Ala Thr Thr
 20 25 30
 Glu Leu Thr Val Ile Gln Pro Gly Met Ser Gln Ser Glu Ile Asp Gln
 35 40 45
 Lys Ile Gly Arg Phe Leu Glu Arg Thr Gly Asn Ser Val Ala Ala Gln
 50 55 60
 Asn Tyr Leu Ile Ala His Asp Tyr Gln Thr Thr Thr Pro Gln Glu Asn
 65 70 75 80
 Thr Ala Ala Ser Pro Val Gln Pro Thr Asn Thr Leu Asn Pro Ile Thr
 85 90 95
 Asn Gln Ala Gln Thr Asp Arg Asp Asn Gly Gln Asp Thr Ala Ile Gln
 100 105 110
 Asp Ala Gln His Ala Ala Asn Trp Ala Ser Leu Lys Ala Asp Asp Ala

115						120						125					
Gln	His	Ala	Ile	Thr	Val	Ala	Gln	Thr	Asp	Ile	Asp	Ala	Asn	Thr	Ala		
	130					135					140						
Ala	Ile	Thr	Asp	Thr	Arg	Asn	Asp	Val	Ser	Ala	Val	Gln	Ser	Asp	Val		
145					150					155					160		
Thr	Asn	Ile	Lys	Gly	Asp	Val	Ala	His	Ala	Gln	Ser	Thr	Ala	Asp	His		
				165					170					175			
Ala	Asn	Ala	Asn	Ala	Asn	Thr	Ala	Leu	Ile	Asn	Gly	Val	Lys	Leu	Ser		
			180					185					190				
Gly	Ala	Val	Thr	Glu	Asn	Lys	Asn	Asn	Ile	Glu	Gln	Asn	Arg	Ser	Asp		
		195					200					205					
Ile	Ala	Asp	Gln	Gln	Lys	Leu	Leu	Ala	Ser	Asn	Glu	Gln	Lys	Gln	Ile		
	210					215					220						
Val	Arg	Asp	Asn	Gly	Gln	Asp	Thr	Ala	Ile	Gln	Asp	Ala	Gln	His	Ala		
225					230					235					240		
Ala	Asn	Trp	Ala	Ser	Leu	Lys	Ala	Asp	Asp	Ala	Gln	His	Ala	Ile	Thr		
				245					250					255			
Val	Ala	Gln	Thr	Asp	Ile	Asp	Ala	Asn	Lys	Ala	Ala	Ile	Thr	Asp	Ile		
			260					265					270				
Arg	Asn	Asp	Val	Ser	Ala	Val	Gln	Ser	Asp	Val	Thr	Asn	Ile	Lys	Gly		
		275					280					285					
Asp	Val	Ala	His	Ala	Gln	Ser	Thr	Ala	Asp	His	Ala	Asn	Ala	Asn	Ala		
	290						295				300						
Asn	Thr	Ala	Leu	Met	Asn	Gly	Val	Lys	Leu	Ser	Ser	Ala	Val	Thr	Glu		
305					310					315					320		
Asn	Lys	Asn	Asn	Ile	Glu	Gln	Asn	Arg	Ser	Asp	Ile	Ala	Asp	Gln	Gln		
				325					330					335			
Lys	Leu	Leu	Ala	Ser	Asn	Glu	Gln	Lys	Gln	Ile	Val	Arg	Asp	Asn	Gly		
			340					345					350				
Gln	Asp	Thr	Ala	Ile	Gln	Asp	Ala	Gln	His	Ala	Ala	Asn	Trp	Ala	Ser		
		355					360						365				
Met	Lys	Ala	Asp	Asp	Ala	Gln	His	Ala	Ile	Thr	Val	Ala	Gln	Thr	Asp		
	370					375					380						
Ile	Asp	Ala	Asn	Lys	Ala	Ala	Ile	Ala	Asp	Thr	Arg	Asn	Asp	Val	Ser		
385					390					395					400		
Ala	Val	Gln	Ser	Asp	Val	Thr	Asn	Ile	Lys	Gly	Asp	Val	Ala	His	Ala		
				405					410					415			
Gln	Ser	Thr	Ala	Asp	His	Ala	Asn	Ala	Asn	Ala	Asn	Thr	Ala	Leu	Ile		
			420					425					430				
Asn	Gly	Val	Lys	Leu	Ser	Gly	Ala	Val	Thr	Glu	Asn	Lys	Asn	Asn	Ile		
		435					440					445					
Glu	Gln	Asn	Arg	Ser	Asp	Ile	Ala	Asp	Gln	Gln	Gln	Gln	Leu	Asp	Glu		

450					455					460					
Thr	Arg	Lys	Ile	Val	Ala	Ala	Thr	Gly	Asp	Val	Gln	Thr	Ala	Ala	Arg
465					470					475					480
Tyr	Gln	Ser	Met	Ile	Asp	Ala	Arg	Gln	Thr	Ala	Ala	Ala	Asn	Ala	Gln
				485					490					495	
Gln	Ala	Gln	Ala	Asp	Thr	Gln	Gln	Gln	Gln	Met	Asp	Asp	Gln	Gln	Lys
			500					505					510		
Gln	Ile	Asp	Ala	Thr	Gln	Lys	Thr	Val	Ser	Ala	Leu	Gly	Asp	Ala	Gln
		515					520					525			
Thr	Asn	Ala	His	Tyr	Gln	Glu	Met	Val	Asn	Ala	Gly	Leu	Arg	Ala	Gln
	530					535					540				
Asn	Asp	Ala	Asn	Ala	Arg	Thr	Ala	Ala	Glu	Gln	Lys	Gln	Lys	Ile	Asp
545					550					555					560
Thr	Leu	Ala	Thr	Asn	Gln	Ala	Thr	Gln	Gln	His	Ile	Asn	Ser	Val	Gln
				565					570					575	
Tyr	Gly	Glu	Gln	Ile	Gln	Arg	Leu	Ala	Gln	Asp	Ser	Thr	Gln	Thr	His
			580					585					590		
Glu	Gln	Ile	Asp	Ser	Leu	Thr	Gln	Asp	Val	Thr	Gln	Thr	His	Gln	Gln
		595					600					605			
Leu	Ser	Asn	Thr	Gln	Lys	Arg	Val	Ala	Asp	Asn	Ser	Gln	Gln	Ile	Thr
	610					615					620				
Thr	Leu	Asn	Asn	His	Phe	Ser	Ser	Leu	Lys	Asn	Glu	Val	Glu	Asp	Asn
625					630					635					640
Arg	Lys	Glu	Ala	Asn	Ala	Gly	Thr	Ala	Ser	Ala	Ile	Ala	Ile	Ala	Ser
				645					650					655	
Gln	Pro	Gln	Val	Lys	Ala	Gly	Asp	Phe	Met	Met	Met	Ser	Ala	Gly	Ala
			660					665					670		
Gly	Thr	Phe	Asn	Gly	Glu	Ser	Ala	Val	Ser	Val	Gly	Thr	Ser	Phe	Asn
		675					680					685			
Ala	Gly	Thr	His	Thr	Val	Ile	Lys	Ala	Gly	Val	Ser	Ala	Asp	Thr	Gln
	690					695					700				
Ser	Asp	Phe	Gly	Ala	Gly	Val	Gly	Val	Gly	Tyr	Ser	Phe			
705					710					715					

<210> 9
 <211> 1743
 <212> PRT
 <213> Escherichia coli

<400> 9															
Met	Asn	Lys	Ile	Phe	Lys	Val	Ile	Trp	Asn	Pro	Ala	Thr	Gly	Ser	Tyr
1				5					10					15	
Thr	Val	Ala	Ser	Glu	Thr	Ala	Lys	Ser	Arg	Gly	Lys	Lys	Ser	Gly	Arg
			20					25					30		
Ser	Lys	Leu	Leu	Ile	Ser	Ala	Leu	Val	Ala	Gly	Gly	Met	Leu	Ser	Ser
		35					40					45			

Phe Gly Val Gln Ala Gln Ala Gly Arg Asp Asn Gly Gln Gly Val Asn
 50 55 60
 Tyr Gly Gln Gly Thr Gly Thr Gly Trp Val Ala Ile Gly Glu Asp Ala
 65 70 75 80
 Lys Ala Asn Ser Phe Thr Asp Thr Gly Gly Gly Ser Ser Thr Ala Val
 85 90 95
 Gly Tyr His Ser Thr Ala Asp Gly Arg Trp Ser Thr Ala Leu Gly Ala
 100 105 110
 Lys Thr His Ser Leu Gly Glu Ala Ser Val Ala Leu Gly Ile Asn Thr
 115 120 125
 Thr Ser Ala Gly Glu Arg Ser Leu Ala Ile Gly Ala Ser Ala Thr Ser
 130 135 140
 Thr Gly Gly Phe Ser Ile Ala Leu Gly Arg Tyr Ala Asn Ser Val Gly
 145 150 155 160
 Glu Phe Ser Ile Ala Gln Gly Asp His Ala Glu Thr Gly Ala Asp Asp
 165 170 175
 Ala Ile Ala Phe Gly Arg Glu Ser Lys Ala Leu Gly Ile Met Ser Ile
 180 185 190
 Ala Leu Gly Ala Thr Ala Asn Ala Ser Lys Glu Tyr Ala Met Ala Leu
 195 200 205
 Gly Ala Ser Ser Ala Ala Ser Ala Ala Asn Ala Ile Ala Val Gly Arg
 210 215 220
 Asn Ser Ala Ala Ala Gly Val Asp Ser Leu Ala Phe Gly Arg Gln Ser
 225 230 235 240
 Ala Ala Ser Ala Ala Asn Ala Ile Ala Met Gly Ala Glu Ser Lys Ala
 245 250 255
 Ala Glu Asn Ala Thr Ala Val Gly Thr Asn Ala Glu Ala Asn Gly Leu
 260 265 270
 Asn Ser Ile Ala Leu Gly Ser Gly Ser Ile Ala Asp Val Asp Asn Thr
 275 280 285
 Ile Ala Leu Gly Asn Gln Ser Gln Ala Val Ala Ala Gly Ala Ile Ala
 290 295 300
 Ile Gly Gln Gly Asn Lys Ala Asp Gly Ala Asn Ala Ile Ala Leu Gly
 305 310 315 320
 Asn Gly Ser Ile Thr Gly Gly Val Asn Ala Ile Ala Leu Gly Gln Gly
 325 330 335
 Ser Tyr Ala Gly Leu Glu Asn Gly Thr Ala Ile Gly Ala Gln Ala Ser
 340 345 350
 Ala Gln Gly Lys Asn Ser Val Ala Leu Gly Ala Gly Ser Val Ala Thr
 355 360 365
 Asp Ala Asp Thr Val Ser Val Gly Asn Thr Thr Ala Gln Arg Gln Ile
 370 375 380

Val 385	Asn	Met	Ala	Ala	Gly 390	Asp	Ile	Ser	Thr	Thr 395	Ser	Thr	Asp	Ala	Ile 400
Asn	Gly	Ser	Gln	Leu 405	Tyr	Ala	Ile	Ser	Lys 410	Ser	Val	Ala	Asp	Asn 415	Leu
Gly	Gly	Gly	Ala 420	Thr	Val	Asn	Ala	Gln 425	Gly	Val	Val	Thr	Ser 430	Pro	Asn
Tyr	Arg	Leu 435	Lys	Ser	Gly	Ile	Phe 440	Gly	Thr	Val	Gly	Asp 445	Ala	Leu	Thr
Gly 450	Leu	Asp	Asn	Asn	Thr	Leu 455	Gln	Trp	Asp	Ser	Leu 460	Lys	Lys	Ala	Tyr
Ser 465	Ala	Ala	His	Gly	Thr 470	Asp	Thr	Thr	Ser	Thr 475	Ile	Thr	Asn	Val	Lys 480
Asp	Gly	Ala	Ile	Ser 485	Asp	Thr	Ser	Lys	Asp 490	Ala	Val	Asn	Gly	Ser 495	Gln
Leu	Lys	Thr	Thr 500	Asn	Asp	Asn	Val	Ala 505	Thr	Asn	Thr	Ala	Asn 510	Ile	Thr
Thr	Asn	Thr 515	Asn	Ser	Ile	Asn	Thr 520	Leu	Thr	Asp	Ser	Val 525	Gly	Asp	Leu
Lys	Asp 530	Asp	Ala	Leu	Leu	Trp 535	Asn	Gly	Thr	Ala	Phe 540	Ser	Ala	Ala	His
Gly 545	Thr	Glu	Ala	Thr	Ser 550	Lys	Ile	Thr	Asn	Val 555	Lys	Asp	Gly	Asp	Leu 560
Thr	Ala	Gly	Ser	Thr 565	Asp	Ala	Val	Asn	Gly 570	Ser	Gln	Leu	Lys	Thr 575	Thr
Asn	Asp	Asn	Val 580	Ala	Thr	Asn	Thr	Thr 585	Asn	Ile	Thr	Asn	Leu 590	Thr	Asp
Ser	Val	Gly 595	Asp	Leu	Lys	Asp	Asp 600	Ala	Leu	Leu	Trp	Asn 605	Gly	Thr	Ala
Phe 610	Ser	Ala	Ala	His	Gly	Thr 615	Asp	Ala	Thr	Ser	Lys 620	Ile	Thr	Asn	Val
Lys 625	Asp	Gly	Asp	Leu	Thr 630	Ala	Gly	Ser	Thr	Asp 635	Ala	Val	Asn	Gly	Ser 640
Gln	Leu	Lys	Thr	Thr 645	Asn	Asp	Ala	Val	Ala 650	Ala	Asn	Thr	Thr	Asn 655	Ile
Ala	Thr	Asn	Thr 660	Thr	Asn	Ile	Thr	Asn 665	Leu	Thr	Asp	Ala	Val 670	Asp	Ser
Leu	Gly	Asp 675	Asp	Ser	Leu	Leu	Trp 680	Asn	Ala	Thr	Ala	Gly 685	Ala	Phe	Ser
Ala 690	Ala	His	Gly	Thr	Asp	Ala 695	Thr	Ser	Lys	Ile	Thr 700	Asn	Val	Thr	Ala
Gly 705	Asp	Leu	Thr	Ala	Gly 710	Ser	Thr	Asp	Ala	Val 715	Asn	Gly	Ser	Gln	Leu 720

Lys Thr Thr Asn Asp Ala Val Ala Ala Asn Thr Thr Asn Ile Ala Thr
 725 730 735
 Asn Thr Thr Asn Ile Thr Asn Leu Thr Asp Ala Val Asp Ser Leu Gly
 740 745 750
 Asp Asp Ser Leu Leu Trp Asn Ala Thr Ala Gly Ala Phe Ser Ala Ala
 755 760 765
 His Gly Thr Asp Ala Thr Ser Lys Ile Thr Asn Val Lys Asp Gly Asp
 770 775 780
 Leu Thr Ala Gly Ser Thr Asp Ala Val Asn Gly Ser Gln Leu Lys Thr
 785 790 795 800
 Thr Asn Asp Ala Val Ala Ala Asn Thr Thr Asn Ile Ala Thr Asn Thr
 805 810 815
 Thr Asn Ile Thr Asn Leu Thr Asp Ala Val Asp Ser Leu Gly Asp Asp
 820 825 830
 Ser Leu Leu Trp Asn Ala Thr Ala Gly Ala Phe Ser Ala Lys His Gly
 835 840 845
 Thr Asn Gly Thr Asp Ser Lys Ile Thr Asn Leu Leu Ala Gly Thr Val
 850 855 860
 Ser Ser Asp Ser Thr Asp Ala Ile Asn Gly Ser Gln Leu Tyr Gly Leu
 865 870 875 880
 Ala Asp Ser Phe Thr Ser Tyr Leu Gly Gly Gly Ala Asp Ile Ser Asp
 885 890 895
 Ala Gly Val Leu Thr Gly Pro Thr Tyr Thr Ile Gly Gly Thr Asp Tyr
 900 905 910
 Asn Asn Val Gly Asp Ala Leu Ala Ala Ile Asn Thr Ser Phe Ser Thr
 915 920 925
 Ser Leu Gly Asp Ala Leu Leu Trp Asp Ala Thr Ala Lys Gly Gly Asp
 930 935 940
 Gly Ala Phe Ser Ala Gly Arg Gly Thr Asp Asn Thr Ala Ser Ile Ile
 945 950 955 960
 Thr Asn Val Ala Asp Gly Ala Ile Ser Ser Thr Ser Ser Asp Ala Ile
 965 970 975
 Asn Gly Ser Gln Leu Tyr Asp Thr Ser Lys Tyr Ile Ala Asp Thr Leu
 980 985 990
 Gly Gly Asp Ala Glu Val Asn Ala Asp Gly Thr Ile Thr Ala Pro Thr
 995 1000 1005
 Tyr Ala Ile Ala Gly Gly Ser Tyr Ser Asn Val Gly Asp Ala Leu Glu
 1010 1015 1020
 Ala Ile Asp Thr Thr Leu Asp Asp Ala Leu Leu Trp Asp Ala Thr Ala
 1025 1030 1035 1040
 Asn Asp Gly Asn Gly Ala Phe Ser Ala Ala His Gly Lys Asp Lys Thr
 1045 1050 1055

Ala Ser Val Ile Thr Asn Val Ala Asn Gly Ala Ile Ser Ala Thr Ser
 1060 1065 1070
 Ser Asp Ala Ile Asn Gly Ser Gln Leu Tyr Thr Thr Asn Lys Tyr Ile
 1075 1080 1085
 Ala Asp Ala Leu Gly Gly Asp Ala Glu Val Asn Ala Asp Gly Ser Ile
 1090 1095 1100
 Thr Ala Pro Thr Tyr Thr Ile Ala Asn Ala Glu Tyr Asn Asn Val Gly
 1105 1110 1115 1120
 Asp Ala Leu Asp Ala Leu Asp Asp Asn Ala Leu Leu Trp Asp Ala Thr
 1125 1130 1135
 Ala Asn Asp Gly Ala Gly Ala Tyr Asn Ala Ser His Asp Gly Lys Ala
 1140 1145 1150
 Ser Ile Ile Thr Asn Val Ala Asp Gly Asn Ile Gly Glu Gly Ser Thr
 1155 1160 1165
 Asp Ala Ile Asn Gly Ser Gln Leu Phe Asn Thr Asn Met Leu Ile Gln
 1170 1175 1180
 Gln Asn Ser Glu Ile Ile Asn Gln Leu Ala Gly Asn Thr Ser Glu Thr
 1185 1190 1195 1200
 Tyr Ile Glu Asp Asn Gly Ala Gly Ile Asn Tyr Val Arg Thr Asn Asp
 1205 1210 1215
 Asn Gly Leu Ala Phe Asn Asp Ala Ser Ala Ser Gly Ile Gly Ala Thr
 1220 1225 1230
 Ala Val Gly Tyr Asn Ala Val Ala Ser Gly Glu Ser Ser Val Ala Ile
 1235 1240 1245
 Gly Gln Gly Ser Ser Ser Asn Val Asp Thr Gly Ile Ala Leu Gly Ser
 1250 1255 1260
 Ser Ser Val Ser Ser Arg Val Ile Val Lys Gly Ser Arg Asp Thr Ser
 1265 1270 1275 1280
 Val Ser Glu Glu Gly Val Val Ile Gly Tyr Asp Thr Thr Asp Gly Glu
 1285 1290 1295
 Leu Leu Gly Ala Leu Ser Ile Gly Asp Asp Gly Lys Tyr Arg Gln Ile
 1300 1305 1310
 Ile Asn Val Ala Asp Gly Ser Glu Ala His Asp Ala Val Thr Val Arg
 1315 1320 1325
 Gln Leu Gln Asn Ala Ile Gly Ala Val Ala Thr Thr Pro Thr Lys Tyr
 1330 1335 1340
 Phe His Ala Asn Ser Thr Glu Glu Asp Ser Leu Ala Val Gly Glu Asp
 1345 1350 1355 1360
 Ser Leu Ala Met Gly Ala Lys Thr Ile Val Asn Gly Asn Ala Gly Ile
 1365 1370 1375
 Gly Ile Gly Tyr Gly Ala Tyr Val Asp Ala Asn Ala Leu Asn Gly Ile
 1380 1385 1390
 Ala Ile Gly Ser Asn Ala Arg Ala Asn His Ala Asn Ser Ile Ala Met

1395	1400	1405
Gly Asn Gly Ser Gln Thr Thr Arg Gly Ala Gln Thr Gly Tyr Ala Ala 1410 1415 1420		
Tyr Asn Met Asp Ala Pro Gln Asn Ser Val Gly Glu Phe Ser Val Gly 1425 1430 1435 1440		
Ser Glu Asp Gly Gln Arg Gln Ile Thr Asn Val Ala Ala Gly Ser Ala 1445 1450 1455		
Asp Thr Asp Ala Val Asn Val Gly Gln Leu Lys Val Thr Asp Ala Gln 1460 1465 1470		
Val Ser Gln Asn Thr Gln Ser Ile Thr Asn Leu Asn Asn Gln Val Thr 1475 1480 1485		
Asn Leu Asp Thr Arg Val Thr Asn Ile Glu Asn Gly Ile Gly Asp Ile 1490 1495 1500		
Val Thr Thr Gly Ser Thr Lys Tyr Phe Lys Thr Asn Thr Asp Gly Val 1505 1510 1515 1520		
Asp Ala Asn Ala Gln Gly Lys Asp Ser Val Ala Ile Gly Ser Gly Ser 1525 1530 1535		
Ile Ala Ala Ala Asp Asn Ser Val Ala Leu Gly Thr Gly Ser Val Ala 1540 1545 1550		
Asn Glu Glu Asn Thr Ile Ser Val Gly Ser Ser Thr Asn Gln Arg Arg 1555 1560 1565		
Ile Thr Asn Val Ala Ala Gly Val Asn Ala Thr Asp Ala Val Asn Val 1570 1575 1580		
Ser Gln Leu Lys Ser Ser Glu Ala Gly Gly Val Arg Tyr Asp Thr Lys 1585 1590 1595 1600		
Ala Asp Gly Ser Val Asp Tyr Ser Asn Ile Thr Leu Gly Gly Gly Asn 1605 1610 1615		
Gly Gly Thr Thr Arg Ile Ser Asn Val Ser Ala Gly Val Asn Asn Asn 1620 1625 1630		
Asp Ala Val Asn Tyr Ala Gln Leu Lys Gln Ser Val Gln Glu Thr Lys 1635 1640 1645		
Gln Tyr Thr Asp Gln Arg Met Val Glu Met Asp Asn Lys Leu Ser Lys 1650 1655 1660		
Thr Glu Ser Lys Leu Ser Gly Gly Ile Ala Ser Ala Met Ala Met Thr 1665 1670 1675 1680		
Gly Leu Pro Gln Ala Tyr Thr Pro Gly Ala Ser Met Ala Ser Ile Gly 1685 1690 1695		
Gly Gly Thr Tyr Asn Gly Glu Ser Ala Val Ala Leu Gly Val Ser Met 1700 1705 1710		
Val Ser Ala Asn Gly Arg Trp Val Tyr Lys Leu Gln Gly Ser Thr Asn 1715 1720 1725		
Ser Gln Gly Glu Tyr Ser Ala Ala Leu Gly Ala Gly Ile Gln Trp 1730 1735 1740		

<210> 10
 <211> 4684
 <212> PRT
 <213> Escherichia coli

<400> 10

Met	Asn	Lys	Lys	Val	Trp	Asn	Ala	Thr	Gly	Ser	Tyr	Thr	Val	Ala	Ser
1				5					10					15	
Thr	Ala	Lys	Ser	Arg	Gly	Lys	Lys	Ser	Gly	Arg	Ser	Lys	Ser	Ala	Val
			20					25					30		
Ala	Gly	Gly	Ser	Ser	Gly	Ala	Ser	Ala	Asp	Asn	Tyr	Thr	Gly	Thr	Asp
		35					40					45			
Tyr	Gly	Asp	Gly	Ser	Ala	Gly	Asp	Gly	Trp	Val	Ala	Gly	Lys	Gly	Ala
	50					55					60				
Lys	Ala	Asn	Thr	Met	Asn	Thr	Ser	Gly	Ala	Ser	Thr	Ala	Gly	Tyr	Asp
65					70					75					80
Ala	Ala	Gly	Tyr	Ser	Ser	Ala	Gly	Ser	Lys	Thr	Ala	Thr	Gly	Gly	Ala
				85					90					95	
Ser	Met	Ala	Gly	Val	Ser	Ala	Lys	Ala	Met	Gly	Asp	Arg	Ser	Val	Ala
			100					105					110		
Gly	Ala	Ser	Ser	Val	Ala	Asn	Gly	Asp	Arg	Ser	Met	Ala	Gly	Arg	Tyr
		115					120					125			
Ala	Lys	Thr	Asn	Gly	Thr	Ser	Ala	Gly	Asp	Ser	Ser	Ala	Asp	Gly	Lys
	130					135						140			
Thr	Ala	Gly	Asn	Thr	Ala	Lys	Ala	Tyr	Met	Ser	Ala	Gly	Asp	Asn	Ala
145					150					155					160
Asn	Ala	Ser	Lys	Tyr	Ala	Met	Ala	Gly	Ala	Ser	Ser	Lys	Ala	Gly	Gly
				165					170					175	
Ala	Asp	Ser	Ala	Gly	Arg	Lys	Ser	Thr	Ala	Asn	Ser	Thr	Gly	Ser	Ala
			180					185					190		
Gly	Ala	Asp	Ser	Ser	Ser	Ser	Asn	Asp	Asn	Ala	Ala	Gly	Asn	Lys	Thr
		195					200					205			
Ala	Gly	Val	Asn	Ser	Met	Ala	Gly	Asn	Ala	Ser	Ala	Ser	Gly	Ser	Ser
	210					215					220				
Ala	Gly	Asn	Thr	Ser	Ala	Ser	Asn	Ala	Ala	Gly	Gly	Ser	Ala	Ser	Lys
225					230					235					240
Val	Asn	Ser	Ala	Gly	Ser	Asn	Ser	Ser	Ser	Gly	Asn	Ala	Ala	Gly	Gly
				245					250					255	
Ser	Ala	Ala	Gly	Gly	Ser	Asn	Ser	Ala	Gly	Ser	Ser	Arg	Ala	Asn	Gly
			260					265					270		
Asn	Asp	Ser	Val	Ala	Gly	Val	Gly	Ala	Ala	Ala	Ala	Thr	Asp	Asn	Ser
		275					280					285			
Val	Ala	Gly	Ala	Gly	Ser	Thr	Thr	Asp	Ala	Ser	Asn	Thr	Val	Ser	Val
	290					295					300				

Gly Asn Ser Ala Thr Lys Arg Lys Val Asn Met Ala Ala Gly Ala Ser
 305 310 315 320
 Asn Thr Ser Thr Asp Ala Asn Gly Ser Tyr Thr Ser Asp Ser Val Ala
 325 330 335
 Lys Arg Gly Gly Gly Ala Thr Val Gly Ser Asp Gly Thr Val Thr Ala
 340 345 350
 Val Ser Tyr Ala Arg Ser Gly Thr Tyr Asn Asn Val Gly Asp Ala Ser
 355 360 365
 Gly Asp Asn Asn Thr Trp Asn Lys Thr Ala Gly Ala Ser Ala Asn His
 370 375 380
 Gly Ala Asn Ala Thr Asn Lys Thr Asn Val Ala Lys Gly Thr Val Ser
 385 390 395 400
 Ala Thr Ser Thr Asp Val Val Asn Gly Ser Tyr Asp Asp Ala Trp Asn
 405 410 415
 Gly Thr Ala Ser Ala Ala His Gly Thr Ala Thr Ser Lys Thr Asn Val
 420 425 430
 Thr Ala Gly Asn Thr Ala Gly Ser Thr Asp Ala Val Asn Gly Ser Lys
 435 440 445
 Thr Thr Asn Asp Asn Val Thr Thr Asn Thr Thr Asn Ala Thr Asn Thr
 450 455 460
 Thr Asn Thr Asn Thr Asp Ala Val Asn Gly Gly Asp Asp Ser Trp Asn
 465 470 475 480
 Lys Ala Ala Gly Ala Ser Ala Ala His Gly Thr Ala Thr Ser Lys Thr
 485 490 495
 Asn Val Thr Ala Gly Asn Thr Ala Gly Ser Thr Asp Ala Val Asn Gly
 500 505 510
 Ser Lys Thr Thr Asn Asp Asn Val Thr Thr Asn Thr Thr Asn Ala Thr
 515 520 525
 Asn Thr Thr Asn Thr Asn Thr Asp Ala Val Asn Gly Gly Asp Asp Ser
 530 535 540
 Trp Asn Lys Thr Ala Gly Ala Ser Ala Ala His Gly Thr Asp Ala Thr
 545 550 555 560
 Ser Lys Thr Asn Val Thr Ala Gly Asn Thr Ala Gly Ser Thr Asp Ala
 565 570 575
 Val Asn Gly Ser Lys Thr Thr Asn Asp Asn Val Thr Thr Asn Thr Thr
 580 585 590
 Asn Ala Thr Asn Thr Thr Asn Thr Asn Thr Asp Ala Val Asn Gly Gly
 595 600 605
 Asp Asp Ser Trp Asn Lys Thr Ala Gly Ala Ser Ala Ala His Gly Thr
 610 615 620
 Asp Ala Thr Ser Lys Thr Asn Val Lys Ala Gly Asp Thr Ala Gly Ser
 625 630 635 640

Thr Asp Ala Val Asn Gly Ser Lys Thr Thr Asn Asp Asn Val Ser Thr
 645 650 655
 Asn Thr Thr Asn Thr Asn Thr Asp Ala Val Asn Gly Gly Asp Asp Ser
 660 665 670
 Trp Asn Lys Thr Ala Gly Ala Ser Ala Ala His Gly Thr Asp Ala Thr
 675 680 685
 Ser Lys Thr Asn Val Lys Ala Gly Asp Thr Ala Gly Ser Thr Asp Ala
 690 695 700
 Val Asn Gly Ser Lys Thr Thr Asn Asp Asn Val Ser Thr Asn Thr Thr
 705 710 715 720
 Asn Thr Asn Thr Asp Ser Val Gly Asp Lys Asp Asp Ser Trp Asn Lys
 725 730 735
 Ala Ala Gly Ala Ser Ala Ala His Gly Thr Ala Thr Ser Lys Thr Asn
 740 745 750
 Ala Gly Lys Ser Ser Asn Ser Thr Asp Ala Asn Gly Ser Tyr Gly Val
 755 760 765
 Ala Asp Ser Thr Ser Tyr Gly Gly Gly Ala Asp Ser Asp Thr Gly Val
 770 775 780
 Ser Gly Thr Tyr Thr Gly Gly Thr Asp Tyr Thr Asn Val Gly Asp Ala
 785 790 795 800
 Ala Ala Asn Thr Ser Ser Thr Ser Gly Asp Ala Trp Asp Ala Thr Ala
 805 810 815
 Gly Lys Ser Ala Lys His Gly Asn Asn Ala Ser Val Thr Asp Val Ala
 820 825 830
 Asn Gly Ala Val Ser Ser Thr Ser Ser Asp Ala Asn Gly Ser Tyr Gly
 835 840 845
 Val Ser Asp Tyr Ala Asp Ala Gly Gly Asn Ala Val Val Asn Thr Asp
 850 855 860
 Gly Ser Thr Thr Thr Tyr Ala Ala Gly Gly Ser Tyr Asn Asn Val Gly
 865 870 875 880
 Asp Ala Ala Asp Thr Thr Asp Asp Ala Trp Asp Thr Thr Ala Asn Gly
 885 890 895
 Gly Asn Gly Ala Ser Ala Ala His Gly Lys Asp Lys Thr Ala Ser Val
 900 905 910
 Thr Asn Val Ala Asn Gly Ala Val Ser Ala Thr Ser Asn Asp Ala Asn
 915 920 925
 Gly Ser Tyr Ser Thr Asn Lys Tyr Ala Asp Ala Gly Gly Asp Ala Val
 930 935 940
 Asn Ala Asp Gly Thr Thr Ala Thr Tyr Thr Ala Asn Thr Asp Tyr Asn
 945 950 955 960
 Asn Val Gly Ala Asp Ala Asp Asn Asn Ala Trp Asp Asp Ala Gly Ala
 965 970 975

Tyr Asn Ala Ser His Asp Gly Asn Ala Ser Lys Thr Asn Val Ala Ala
 980 985 990
 Gly Asp Ser Thr Thr Ser Thr Asp Ala Val Asn Gly Ser Asn Ala Thr
 995 1000 1005
 Asn Val Thr Asn Ser Met Asn Ala Gly Asn Thr Ser Thr Tyr Asn Gly
 1010 1015 1020
 Ala Gly Asn Tyr Val Arg Thr Asn Asp Ser Gly Ala Asn Asp Ala Ser
 1025 1030 1035 1040
 Ala Ser Gly Gly Ala Thr Ala Val Gly Tyr Asn Ala Val Ala Ser His
 1045 1050 1055
 Ala Ser Ser Val Ala Gly Asp Ser Ser Val Asp Thr Gly Ala Gly Ser
 1060 1065 1070
 Ser Ser Val Ser Ser Arg Val Val Lys Gly Thr Arg Asn Thr Ser Val
 1075 1080 1085
 Ser Gly Val Val Gly Tyr Asp Thr Thr Asp Gly Gly Ala Ser Gly Asp
 1090 1095 1100
 Asp Gly Lys Tyr Arg Asn Val Ala Asp Gly Ser Ala His Asp Ala Val
 1105 1110 1115 1120
 Thr Val Arg Asn Ala Gly Ala Val Ala Thr Thr Thr Lys Tyr Tyr His
 1125 1130 1135
 Ala Asn Ser Thr Ala Asp Ser Ala Val Gly Asp Ser Ala Met Gly Ala
 1140 1145 1150
 Lys Thr Val Asn Gly Asn Ala Gly Gly Gly Asn Thr Val Ala Asp Ala
 1155 1160 1165
 Asn Gly Ala Gly Ser Asn Ala Arg Ala Asn His Ala Asp Ser Ala Met
 1170 1175 1180
 Gly Asn Gly Ser Thr Thr Arg Gly Ala Thr Asn Tyr Thr Ala Tyr Asn
 1185 1190 1195 1200
 Met Asp Ala Asn Ser Val Gly Ser Val Gly Ser Asp Gly Arg Thr Asn
 1205 1210 1215
 Val Ala Ala Gly Ser Ala Asp Thr Asp Ala Val Asn Val Gly Lys Val
 1220 1225 1230
 Thr Asp Ala Val Ser Asn Thr Ser Thr Asn Asn Thr Val Thr Asn Asp
 1235 1240 1245
 Thr Arg Val Thr Asn Asn Gly Gly Asp Val Thr Thr Gly Ser Thr Lys
 1250 1255 1260
 Tyr Lys Thr Asn Thr Asp Gly Ala Asp Ala Asn Ala Gly Lys Asp Ser
 1265 1270 1275 1280
 Val Ala Gly Ser Gly Ser Ala Ala Ala Asp Asn Ser Val Ala Gly Thr
 1285 1290 1295
 Gly Ser Val Ala Asp Asn Thr Ser Val Gly Ser Ser Thr Asn Arg Arg
 1300 1305 1310
 Thr Asn Val Ala Ala Gly Val Asn Ala Thr Asp Ala Val Asn Val Ser

1315	1320	1325
Lys Ser Ser Ala Gly Gly Val Arg Tyr Asp Thr	Lys Ala Asp Gly Ser	
1330	1335	1340
Asp Tyr Ser Asn Thr Gly Gly Gly Asn Ser Gly Thr Thr Arg Ser Asn		
1345	1350	1355 1360
Val Ser Ala Gly Val Asn Asn Asn Asp Ala Val Asn Tyr Ala Lys Ser		
1365	1370	1375
Val Thr Lys Tyr Thr Asp Arg Met Val Met Asp Asn Lys Ser Lys Thr		
1380	1385	1390
Ser Lys Ser Gly Gly Ala Ser Ala Met Ala Met Thr Gly Ala Tyr Thr		
1395	1400	1405
Gly Ala Ser Met Ala Ser Gly Gly Gly Thr Tyr Asn Gly Ser Ala Val		
1410	1415	1420
Ala Gly Val Ser Met Val Ser Ala Asn Gly Arg Trp Val Tyr Lys Gly		
1425	1430	1435 1440
Ser Thr Asn Ser Gly Tyr Ser Ala Ala Gly Ala Gly Trp Met Asn Lys		
1445	1450	1455
Lys Val Trp Asn Ala Thr Gly Ser Tyr Thr Val Ala Ser Thr Ala Lys		
1460	1465	1470
Ser Arg Gly Lys Lys Ser Gly Arg Ser Lys Ser Ala Val Ala Gly Gly		
1475	1480	1485
Ser Ser Gly Ala Ser Ala Asp Asn Tyr Thr Gly Thr Asp Tyr Gly Asp		
1490	1495	1500
Gly Ser Ala Gly Asp Gly Trp Val Ala Gly Lys Gly Ala Lys Ala Asn		
1505	1510	1515 1520
Thr Met Asn Thr Ser Gly Ala Ser Thr Ala Gly Tyr Asp Ala Ala Gly		
1525	1530	1535
Tyr Ser Ser Ala Gly Ser Lys Thr Ala Thr Gly Gly Ala Ser Met Ala		
1540	1545	1550
Gly Val Ser Ala Lys Ala Met Gly Asp Arg Ser Val Ala Gly Ala Ser		
1555	1560	1565
Ser Val Ala Asn Gly Asp Arg Ser Met Ala Gly Arg Tyr Ala Lys Thr		
1570	1575	1580
Asn Gly Thr Ser Ala Gly Asp Ser Ser Ala Asp Gly Lys Thr Ala Gly		
1585	1590	1595 1600
Asn Thr Ala Lys Ala Tyr Met Ser Ala Gly Asp Asn Ala Asn Ala Ser		
1605	1610	1615
Lys Tyr Ala Met Ala Gly Ala Ser Ser Lys Ala Gly Gly Ala Asp Ser		
1620	1625	1630
Ala Gly Arg Lys Ser Thr Ala Asn Ser Thr Gly Ser Ala Gly Ala Asp		
1635	1640	1645
Ser Ser Ser Ser Asn Asp Asn Ala Ala Gly Asn Lys Thr Ala Gly Val		

1650					1655					1660					
Asn	Ser	Met	Ala	Gly	Asn	Ala	Ser	Ala	Ser	Gly	Ser	Ser	Ala	Gly	Asn
1665					1670					1675					1680
Thr	Ser	Ala	Ser	Asn	Ala	Ala	Gly	Gly	Ser	Ala	Ser	Lys	Val	Asn	Ser
				1685					1690					1695	
Ala	Gly	Ser	Asn	Ser	Ser	Ser	Gly	Asn	Ala	Ala	Gly	Gly	Ser	Ala	Ala
			1700					1705					1710		
Gly	Gly	Ser	Asn	Ser	Ala	Gly	Ser	Ser	Arg	Ala	Asn	Gly	Asn	Asp	Ser
		1715					1720					1725			
Val	Ala	Gly	Val	Gly	Ala	Ala	Ala	Ala	Thr	Asp	Asn	Ser	Val	Ala	Gly
	1730					1735					1740				
Ala	Gly	Ser	Thr	Thr	Asp	Ala	Ser	Asn	Thr	Val	Ser	Val	Gly	Asn	Ser
1745					1750				1755					1760	
Ala	Thr	Lys	Arg	Lys	Val	Asn	Met	Ala	Ala	Gly	Ala	Ser	Asn	Thr	Ser
				1765				1770						1775	
Thr	Asp	Ala	Asn	Gly	Ser	Tyr	Thr	Ser	Asp	Ser	Val	Ala	Lys	Arg	Gly
			1780					1785					1790		
Gly	Gly	Ala	Thr	Val	Gly	Ser	Asp	Gly	Thr	Val	Thr	Ala	Val	Ser	Tyr
		1795					1800					1805			
Ala	Arg	Ser	Gly	Thr	Tyr	Asn	Asn	Val	Gly	Asp	Ala	Ser	Gly	Asp	Asn
	1810					1815					1820				
Asn	Thr	Trp	Asn	Lys	Thr	Ala	Gly	Ala	Ser	Ala	Asn	His	Gly	Ala	Asn
1825					1830				1835					1840	
Ala	Thr	Asn	Lys	Thr	Asn	Val	Ala	Lys	Gly	Thr	Val	Ser	Ala	Thr	Ser
			1845					1850						1855	
Thr	Asp	Val	Val	Asn	Gly	Ser	Tyr	Asp	Asp	Ala	Trp	Asn	Gly	Thr	Ala
			1860					1865					1870		
Ser	Ala	Ala	His	Gly	Thr	Ala	Thr	Ser	Lys	Thr	Asn	Val	Thr	Ala	Gly
		1875				1880					1885				
Asn	Thr	Ala	Gly	Ser	Thr	Asp	Ala	Val	Asn	Gly	Ser	Lys	Thr	Thr	Asn
	1890					1895					1900				
Asp	Asn	Val	Thr	Thr	Asn	Thr	Thr	Asn	Ala	Thr	Asn	Thr	Thr	Asn	Thr
1905					1910				1915					1920	
Asn	Thr	Asp	Ala	Val	Asn	Gly	Gly	Asp	Asp	Ser	Trp	Asn	Lys	Ala	Ala
			1925					1930						1935	
Gly	Ala	Ser	Ala	Ala	His	Gly	Thr	Ala	Thr	Ser	Lys	Thr	Asn	Val	Thr
			1940					1945					1950		
Ala	Gly	Asn	Thr	Ala	Gly	Ser	Thr	Asp	Ala	Val	Asn	Gly	Ser	Lys	Thr
		1955					1960					1965			
Thr	Asn	Asp	Asn	Val	Thr	Thr	Asn	Thr	Thr	Asn	Ala	Thr	Asn	Thr	Thr
			1970				1975				1980				
Asn	Thr	Asn	Thr	Asp	Ala	Val	Asn	Gly	Gly	Asp	Asp	Ser	Trp	Asn	Lys
1985					1990					1995				2000	

Thr Ala Gly Ala Ser Ala Ala His Gly Thr Asp Ala Thr Ser Lys Thr
 2005 2010 2015
 Asn Val Thr Ala Gly Asn Thr Ala Gly Ser Thr Asp Ala Val Asn Gly
 2020 2025 2030
 Ser Lys Thr Thr Asn Asp Asn Val Thr Thr Asn Thr Thr Asn Ala Thr
 2035 2040 2045
 Asn Thr Thr Asn Thr Asn Thr Asp Ala Val Asn Gly Gly Asp Asp Ser
 2050 2055 2060
 Trp Asn Lys Thr Ala Gly Ala Ser Ala Ala His Gly Thr Asp Ala Thr
 2065 2070 2075 2080
 Ser Lys Thr Asn Val Lys Ala Gly Asp Thr Ala Gly Ser Thr Asp Ala
 2085 2090 2095
 Val Asn Gly Ser Lys Thr Thr Asn Asp Asn Val Ser Thr Asn Thr Thr
 2100 2105 2110
 Asn Thr Asn Thr Asp Ala Val Asn Gly Gly Asp Asp Ser Trp Asn Lys
 2115 2120 2125
 Thr Ala Gly Ala Ser Ala Ala His Gly Thr Asp Ala Thr Ser Lys Thr
 2130 2135 2140
 Asn Val Lys Ala Gly Asp Thr Ala Gly Ser Thr Asp Ala Val Asn Gly
 2145 2150 2155 2160
 Ser Lys Thr Thr Asn Asp Asn Val Ser Thr Asn Thr Thr Asn Thr Asn
 2165 2170 2175
 Thr Asp Ser Val Gly Asp Lys Asp Asp Ser Trp Asn Lys Ala Ala Gly
 2180 2185 2190
 Ala Ser Ala Ala His Gly Thr Ala Thr Ser Lys Thr Asn Ala Gly Lys
 2195 2200 2205
 Ser Ser Asn Ser Thr Asp Ala Asn Gly Ser Tyr Gly Val Ala Asp Ser
 2210 2215 2220
 Thr Ser Tyr Gly Gly Gly Ala Asp Ser Asp Thr Gly Val Ser Gly Thr
 2225 2230 2235 2240
 Tyr Thr Gly Gly Thr Asp Tyr Thr Asn Val Gly Asp Ala Ala Ala Asn
 2245 2250 2255
 Thr Ser Ser Thr Ser Gly Asp Ala Trp Asp Ala Thr Ala Gly Lys Ser
 2260 2265 2270
 Ala Lys His Gly Asn Asn Ala Ser Val Thr Asp Val Ala Asn Gly Ala
 2275 2280 2285
 Val Ser Ser Thr Ser Ser Asp Ala Asn Gly Ser Tyr Gly Val Ser Asp
 2290 2295 2300
 Tyr Ala Asp Ala Gly Gly Asn Ala Val Val Asn Thr Asp Gly Ser Thr
 2305 2310 2315 2320
 Thr Thr Tyr Ala Ala Gly Gly Ser Tyr Asn Asn Val Gly Asp Ala Ala
 2325 2330 2335

Asp Thr Thr Asp Asp Ala Trp Asp Thr Thr Ala Asn Gly Gly Asn Gly
 2340 2345 2350
 Ala Ser Ala Ala His Gly Lys Asp Lys Thr Ala Ser Val Thr Asn Val
 2355 2360 2365
 Ala Asn Gly Ala Val Ser Ala Thr Ser Asn Asp Ala Asn Gly Ser Tyr
 2370 2375 2380
 Ser Thr Asn Lys Tyr Ala Asp Ala Gly Gly Asp Ala Val Asn Ala Asp
 2385 2390 2395 2400
 Gly Thr Thr Ala Thr Tyr Thr Ala Asn Thr Asp Tyr Asn Asn Val Gly
 2405 2410 2415
 Ala Asp Ala Asp Asn Asn Ala Trp Asp Asp Ala Gly Ala Tyr Asn Ala
 2420 2425 2430
 Ser His Asp Gly Asn Ala Ser Lys Thr Asn Val Ala Ala Gly Asp Ser
 2435 2440 2445
 Thr Thr Ser Thr Asp Ala Val Asn Gly Ser Asn Ala Thr Asn Val Thr
 2450 2455 2460
 Asn Ser Met Asn Ala Gly Asn Thr Ser Thr Tyr Asn Gly Ala Gly Asn
 2465 2470 2475 2480
 Tyr Val Arg Thr Asn Asp Ser Gly Ala Asn Asp Ala Ser Ala Ser Gly
 2485 2490 2495
 Gly Ala Thr Ala Val Gly Tyr Asn Ala Val Ala Ser His Ala Ser Ser
 2500 2505 2510
 Val Ala Gly Asp Ser Ser Val Asp Thr Gly Ala Gly Ser Ser Ser Val
 2515 2520 2525
 Ser Ser Arg Val Val Lys Gly Thr Arg Asn Thr Ser Val Ser Gly Val
 2530 2535 2540
 Val Gly Tyr Asp Thr Thr Asp Gly Gly Ala Ser Gly Asp Asp Gly Lys
 2545 2550 2555 2560
 Tyr Arg Asn Val Ala Asp Gly Ser Ala His Asp Ala Val Thr Val Arg
 2565 2570 2575
 Asn Ala Gly Ala Val Ala Thr Thr Thr Lys Tyr Tyr His Ala Asn Ser
 2580 2585 2590
 Thr Ala Asp Ser Ala Val Gly Asp Ser Ala Met Gly Ala Lys Thr Val
 2595 2600 2605
 Asn Gly Asn Ala Gly Gly Gly Asn Thr Val Ala Asp Ala Asn Gly Ala
 2610 2615 2620
 Gly Ser Asn Ala Arg Ala Asn His Ala Asp Ser Ala Met Gly Asn Gly
 2625 2630 2635 2640
 Ser Thr Thr Arg Gly Ala Thr Asn Tyr Thr Ala Tyr Asn Met Asp Ala
 2645 2650 2655
 Asn Ser Val Gly Ser Val Gly Ser Asp Gly Arg Thr Asn Val Ala Ala
 2660 2665 2670

Gly Ser Ala Asp Thr Asp Ala Val Asn Val Gly Lys Val Thr Asp Ala
 2675 2680 2685
 Val Ser Asn Thr Ser Thr Asn Asn Thr Val Thr Asn Asp Thr Arg Val
 2690 2695 2700
 Thr Asn Asn Gly Gly Asp Val Thr Thr Gly Ser Thr Lys Tyr Lys Thr
 2705 2710 2715 2720
 Asn Thr Asp Gly Ala Asp Ala Asn Ala Gly Lys Asp Ser Val Ala Gly
 2725 2730 2735
 Ser Gly Ser Ala Ala Ala Asp Asn Ser Val Ala Gly Thr Gly Ser Val
 2740 2745 2750
 Ala Asp Asn Thr Ser Val Gly Ser Ser Thr Asn Arg Arg Thr Asn Val
 2755 2760 2765
 Ala Ala Gly Val Asn Ala Thr Asp Ala Val Asn Val Ser Lys Ser Ser
 2770 2775 2780
 Ala Gly Gly Val Arg Tyr Asp Thr Lys Ala Asp Gly Ser Asp Tyr Ser
 2785 2790 2795 2800
 Asn Thr Gly Gly Gly Asn Ser Gly Thr Thr Arg Ser Asn Val Ser Ala
 2805 2810 2815
 Gly Val Asn Asn Asn Asp Ala Val Asn Tyr Ala Lys Ser Val Thr Lys
 2820 2825 2830
 Tyr Thr Asp Arg Met Val Met Asp Asn Lys Ser Lys Thr Ser Lys Ser
 2835 2840 2845
 Gly Gly Ala Ser Ala Met Ala Met Thr Gly Ala Tyr Thr Gly Ala Ser
 2850 2855 2860
 Met Ala Ser Gly Gly Gly Thr Tyr Asn Gly Ser Ala Val Ala Gly Val
 2865 2870 2875 2880
 Ser Met Val Ser Ala Asn Gly Arg Trp Val Tyr Lys Gly Ser Thr Asn
 2885 2890 2895
 Ser Gly Tyr Ser Ala Ala Gly Ala Gly Trp Met Asn Lys Ile Phe Lys
 2900 2905 2910
 Val Ile Trp Asn Pro Ala Thr Gly Ser Tyr Thr Val Ala Ser Glu Thr
 2915 2920 2925
 Ala Lys Ser Arg Gly Lys Lys Ser Gly Arg Ser Lys Leu Leu Ile Ser
 2930 2935 2940
 Ala Leu Val Ala Gly Gly Leu Leu Ser Ser Phe Gly Ala Ser Ala Asp
 2945 2950 2955 2960
 Asn Tyr Thr Gly Gln Pro Thr Asp Tyr Gly Asp Gly Ser Ala Gly Asp
 2965 2970 2975
 Gly Trp Val Ala Ile Gly Lys Gly Ala Lys Ala Asn Thr Phe Met Asn
 2980 2985 2990
 Thr Ser Gly Ala Ser Thr Ala Leu Gly Tyr Asp Ala Ile Ala Glu Gly
 2995 3000 3005

Glu Tyr Ser Ser Ala Ile Gly Ser Lys Thr Leu Ala Thr Gly Gly Ala
 3010 3015 3020
 Ser Met Ala Phe Gly Val Ser Ala Lys Ala Met Gly Asp Arg Ser Val
 3025 3030 3035 3040
 Ala Leu Gly Ala Ser Ser Val Ala Asn Gly Asp Arg Ser Met Ala Phe
 3045 3050 3055
 Gly Arg Tyr Ala Lys Thr Asn Gly Phe Thr Ser Leu Ala Ile Gly Asp
 3060 3065 3070
 Ser Ser Leu Ala Asp Gly Glu Lys Thr Ile Ala Leu Gly Asn Thr Ala
 3075 3080 3085
 Lys Ala Tyr Glu Ile Met Ser Ile Ala Leu Gly Asp Asn Ala Asn Ala
 3090 3095 3100
 Ser Lys Glu Tyr Ala Met Ala Leu Gly Ala Ser Ser Lys Ala Gly Gly
 3105 3110 3115 3120
 Ala Asp Ser Leu Ala Phe Gly Arg Lys Ser Thr Ala Asn Ser Thr Gly
 3125 3130 3135
 Ser Leu Ala Ile Gly Ala Asp Ser Ser Ser Ser Asn Asp Asn Ala Ile
 3140 3145 3150
 Ala Ile Gly Asn Lys Thr Gln Ala Leu Gly Val Asn Ser Met Ala Leu
 3155 3160 3165
 Gly Asn Ala Ser Gln Ala Ser Gly Glu Ser Ser Ile Ala Leu Gly Asn
 3170 3175 3180
 Thr Ser Glu Ala Ser Glu Gln Asn Ala Ile Ala Leu Gly Gln Gly Ser
 3185 3190 3195 3200
 Ile Ala Ser Lys Val Asn Ser Ile Ala Leu Gly Ser Asn Ser Leu Ser
 3205 3210 3215
 Ser Gly Glu Asn Ala Ile Ala Leu Gly Glu Gly Ser Ala Ala Gly Gly
 3220 3225 3230
 Ser Asn Ser Leu Ala Phe Gly Ser Gln Ser Arg Ala Asn Gly Asn Asp
 3235 3240 3245
 Ser Val Ala Ile Gly Val Gly Ala Ala Ala Ala Thr Asp Asn Ser Val
 3250 3255 3260
 Ala Ile Gly Ala Gly Ser Thr Thr Asp Ala Ser Asn Thr Val Ser Val
 3265 3270 3275 3280
 Gly Asn Ser Ala Thr Lys Arg Lys Ile Val Asn Met Ala Ala Gly Ala
 3285 3290 3295
 Ile Ser Asn Thr Ser Thr Asp Ala Ile Asn Gly Ser Gln Leu Tyr Thr
 3300 3305 3310
 Ile Ser Asp Ser Val Ala Lys Arg Leu Gly Gly Gly Ala Thr Val Gly
 3315 3320 3325
 Ser Asp Gly Thr Val Thr Ala Val Ser Tyr Ala Leu Arg Ser Gly Thr
 3330 3335 3340
 Tyr Asn Asn Val Gly Asp Ala Leu Ser Gly Ile Asp Asn Asn Thr Leu

3345	3350	3355	3360
Gln Trp Asn Lys Thr Ala Gly Ala Phe Ser Ala Asn His Gly Ala Asn	3365	3370	3375
Ala Thr Asn Lys Ile Thr Asn Val Ala Lys Gly Thr Val Ser Ala Thr	3380	3385	3390
Ser Thr Asp Val Val Asn Gly Ser Gln Leu Tyr Asp Leu Gln Gln Asp	3395	3400	3405
Ala Leu Leu Trp Asn Gly Thr Ala Phe Ser Ala Ala His Gly Thr Glu	3410	3415	3420
Ala Thr Ser Lys Ile Thr Asn Val Thr Ala Gly Asn Leu Thr Ala Gly	3425	3430	3435
Ser Thr Asp Ala Val Asn Gly Ser Gln Leu Lys Thr Thr Asn Asp Asn	3445	3450	3455
Val Thr Thr Asn Thr Thr Asn Ile Ala Thr Asn Thr Thr Asn Ile Thr	3460	3465	3470
Asn Leu Thr Asp Ala Val Asn Gly Leu Gly Asp Asp Ser Leu Leu Trp	3475	3480	3485
Asn Lys Ala Ala Gly Ala Phe Ser Ala Ala His Gly Thr Glu Ala Thr	3490	3495	3500
Ser Lys Ile Thr Asn Val Thr Ala Gly Asn Leu Thr Ala Gly Ser Thr	3505	3510	3515
Asp Ala Val Asn Gly Ser Gln Leu Lys Thr Thr Asn Asp Asn Val Thr	3525	3530	3535
Thr Asn Thr Thr Asn Ile Ala Thr Asn Thr Thr Asn Ile Thr Asn Leu	3540	3545	3550
Thr Asp Ala Val Asn Gly Leu Gly Asp Asp Ser Leu Leu Trp Asn Lys	3555	3560	3565
Thr Ala Gly Ala Phe Ser Ala Ala His Gly Thr Asp Ala Thr Ser Lys	3570	3575	3580
Ile Thr Asn Val Thr Ala Gly Asn Leu Thr Ala Gly Ser Thr Asp Ala	3585	3590	3595
Val Asn Gly Ser Gln Leu Lys Thr Thr Asn Asp Asn Val Thr Thr Asn	3605	3610	3615
Thr Thr Asn Ile Ala Thr Asn Thr Thr Asn Ile Thr Asn Leu Thr Asp	3620	3625	3630
Ala Val Asn Gly Leu Gly Asp Asp Ser Leu Leu Trp Asn Lys Thr Ala	3635	3640	3645
Gly Ala Phe Ser Ala Ala His Gly Thr Asp Ala Thr Ser Lys Ile Thr	3650	3655	3660
Asn Val Lys Ala Gly Asp Leu Thr Ala Gly Ser Thr Asp Ala Val Asn	3665	3670	3675
Gly Ser Gln Leu Lys Thr Thr Asn Asp Asn Val Ser Thr Asn Thr Thr			

3685										3690					3695				
Asn	Ile	Thr	Asn	Leu	Thr	Asp	Ala	Val	Asn	Gly	Leu	Gly	Asp	Asp	Ser				
			3700					3705					3710						
Leu	Leu	Trp	Asn	Lys	Thr	Ala	Gly	Ala	Phe	Ser	Ala	Ala	His	Gly	Thr				
			3715				3720					3725							
Asp	Ala	Thr	Ser	Lys	Ile	Thr	Asn	Val	Lys	Ala	Gly	Asp	Leu	Thr	Ala				
	3730					3735					3740								
Gly	Ser	Thr	Asp	Ala	Val	Asn	Gly	Ser	Gln	Leu	Lys	Thr	Thr	Asn	Asp				
3745					3750					3755					3760				
Asn	Val	Ser	Thr	Asn	Thr	Thr	Asn	Ile	Thr	Asn	Leu	Thr	Asp	Ser	Val				
				3765					3770					3775					
Gly	Asp	Leu	Lys	Asp	Asp	Ser	Leu	Leu	Trp	Asn	Lys	Ala	Ala	Gly	Ala				
			3780					3785					3790						
Phe	Ser	Ala	Ala	His	Gly	Thr	Glu	Ala	Thr	Ser	Lys	Ile	Thr	Asn	Leu				
		3795					3800					3805							
Leu	Ala	Gly	Lys	Ile	Ser	Ser	Asn	Ser	Thr	Asp	Ala	Ile	Asn	Gly	Ser				
	3810					3815					3820								
Gln	Leu	Tyr	Gly	Val	Ala	Asp	Ser	Phe	Thr	Ser	Tyr	Leu	Gly	Gly	Gly				
3825					3830					3835					3840				
Ala	Asp	Ile	Ser	Asp	Thr	Gly	Val	Leu	Ser	Gly	Pro	Thr	Tyr	Thr	Ile				
				3845					3850					3855					
Gly	Gly	Thr	Asp	Tyr	Thr	Asn	Val	Gly	Asp	Ala	Leu	Ala	Ala	Ile	Asn				
			3860					3865					3870						
Thr	Ser	Phe	Ser	Thr	Ser	Leu	Gly	Asp	Ala	Leu	Leu	Trp	Asp	Ala	Thr				
		3875					3880					3885							
Ala	Gly	Lys	Phe	Ser	Ala	Lys	His	Gly	Ile	Asn	Asn	Ala	Pro	Ser	Val				
	3890					3895				3900									
Ile	Thr	Asp	Val	Ala	Asn	Gly	Ala	Val	Ser	Ser	Thr	Ser	Ser	Asp	Ala				
3905					3910					3915					3920				
Ile	Asn	Gly	Ser	Gln	Leu	Tyr	Gly	Val	Ser	Asp	Tyr	Ile	Ala	Asp	Ala				
				3925					3930					3935					
Leu	Gly	Gly	Asn	Ala	Val	Val	Asn	Thr	Asp	Gly	Ser	Ile	Thr	Thr	Pro				
			3940					3945						3950					
Thr	Tyr	Ala	Ile	Ala	Gly	Gly	Ser	Tyr	Asn	Asn	Val	Gly	Asp	Ala	Leu				
		3955					3960					3965							
Glu	Ala	Ile	Asp	Thr	Thr	Leu	Asp	Asp	Ala	Leu	Leu	Trp	Asp	Thr	Thr				
	3970					3975					3980								
Ala	Asn	Gly	Gly	Asn	Gly	Ala	Phe	Ser	Ala	Ala	His	Gly	Lys	Asp	Lys				
3985					3990					3995					4000				
Thr	Ala	Ser	Val	Ile	Thr	Asn	Val	Ala	Asn	Gly	Ala	Val	Ser	Ala	Thr				
				4005					4010					4015					
Ser	Asn	Asp	Ala	Ile	Asn	Gly	Ser	Gln	Leu	Tyr	Ser	Thr	Asn	Lys	Tyr				
			4020					4025						4030					

Ile Ala Asp Ala Leu Gly Gly Asp Ala Glu Val Asn Ala Asp Gly Thr
 4035 4040 4045
 Ile Thr Ala Pro Thr Tyr Thr Ile Ala Asn Thr Asp Tyr Asn Asn Val
 4050 4055 4060
 Gly Glu Ala Leu Asp Ala Leu Asp Asn Asn Ala Leu Leu Trp Asp Glu
 4065 4070 4075 4080
 Asp Ala Gly Ala Tyr Asn Ala Ser His Asp Gly Asn Ala Ser Lys Ile
 4085 4090 4095
 Thr Asn Val Ala Ala Gly Asp Leu Ser Thr Thr Ser Thr Asp Ala Val
 4100 4105 4110
 Asn Gly Ser Gln Leu Asn Ala Thr Asn Ile Leu Val Thr Gln Asn Ser
 4115 4120 4125
 Gln Met Ile Asn Gln Leu Ala Gly Asn Thr Ser Glu Thr Tyr Ile Glu
 4130 4135 4140
 Glu Asn Gly Ala Gly Ile Asn Tyr Val Arg Thr Asn Asp Ser Gly Leu
 4145 4150 4155 4160
 Ala Phe Asn Asp Ala Ser Ala Ser Gly Ile Gly Ala Thr Ala Val Gly
 4165 4170 4175
 Tyr Asn Ala Val Ala Ser His Ala Ser Ser Val Ala Ile Gly Gln Asp
 4180 4185 4190
 Ser Ile Ser Glu Val Asp Thr Gly Ile Ala Leu Gly Ser Ser Ser Val
 4195 4200 4205
 Ser Ser Arg Val Ile Val Lys Gly Thr Arg Asn Thr Ser Val Ser Glu
 4210 4215 4220
 Glu Gly Val Val Ile Gly Tyr Asp Thr Thr Asp Gly Glu Leu Leu Gly
 4225 4230 4235 4240
 Ala Leu Ser Ile Gly Asp Asp Gly Lys Tyr Arg Gln Ile Ile Asn Val
 4245 4250 4255
 Ala Asp Gly Ser Glu Ala His Asp Ala Val Thr Val Arg Gln Leu Gln
 4260 4265 4270
 Asn Ala Ile Gly Ala Val Ala Thr Thr Pro Thr Lys Tyr Tyr His Ala
 4275 4280 4285
 Asn Ser Thr Ala Glu Asp Ser Leu Ala Val Gly Glu Asp Ser Leu Ala
 4290 4295 4300
 Met Gly Ala Lys Thr Ile Val Asn Gly Asn Ala Gly Ile Gly Ile Gly
 4305 4310 4315 4320
 Leu Asn Thr Leu Val Leu Ala Asp Ala Ile Asn Gly Ile Ala Ile Gly
 4325 4330 4335
 Ser Asn Ala Arg Ala Asn His Ala Asp Ser Ile Ala Met Gly Asn Gly
 4340 4345 4350
 Ser Gln Thr Thr Arg Gly Ala Gln Thr Asn Tyr Thr Ala Tyr Asn Met
 4355 4360 4365

Asp Ala Pro Gln Asn Ser Val Gly Glu Phe Ser Val Gly Ser Glu Asp
 4370 4375 4380
 Gly Gln Arg Gln Ile Thr Asn Val Ala Ala Gly Ser Ala Asp Thr Asp
 4385 4390 4395 4400
 Ala Val Asn Val Gly Gln Leu Lys Val Thr Asp Ala Gln Val Ser Gln
 4405 4410 4415
 Asn Thr Gln Ser Ile Thr Asn Leu Asn Thr Gln Val Thr Asn Leu Asp
 4420 4425 4430
 Thr Arg Val Thr Asn Ile Glu Asn Gly Ile Gly Asp Ile Val Thr Thr
 4435 4440 4445
 Gly Ser Thr Lys Tyr Phe Lys Thr Asn Thr Asp Gly Ala Asp Ala Asn
 4450 4455 4460
 Ala Gln Gly Lys Asp Ser Val Ala Ile Gly Ser Gly Ser Ile Ala Ala
 4465 4470 4475 4480
 Ala Asp Asn Ser Val Ala Leu Gly Thr Gly Ser Val Ala Asp Glu Glu
 4485 4490 4495
 Asn Thr Ile Ser Val Gly Ser Ser Thr Asn Gln Arg Arg Ile Thr Asn
 4500 4505 4510
 Val Ala Ala Gly Val Asn Ala Thr Asp Ala Val Asn Val Ser Gln Leu
 4515 4520 4525
 Lys Ser Ser Glu Ala Gly Gly Val Arg Tyr Asp Thr Lys Ala Asp Gly
 4530 4535 4540
 Ser Ile Asp Tyr Ser Asn Ile Thr Leu Gly Gly Gly Asn Ser Gly Thr
 4545 4550 4555 4560
 Thr Arg Ile Ser Asn Val Ser Ala Gly Val Asn Asn Asn Asp Ala Val
 4565 4570 4575
 Asn Tyr Ala Gln Leu Lys Gln Ser Val Gln Glu Thr Lys Gln Tyr Thr
 4580 4585 4590
 Asp Gln Arg Met Val Glu Met Asp Asn Lys Leu Ser Lys Thr Glu Ser
 4595 4600 4605
 Lys Leu Ser Gly Gly Ile Ala Ser Ala Met Ala Met Thr Gly Leu Pro
 4610 4615 4620
 Gln Ala Tyr Thr Pro Gly Ala Ser Met Ala Ser Ile Gly Gly Gly Thr
 4625 4630 4635 4640
 Tyr Asn Gly Glu Ser Ala Val Ala Leu Gly Val Ser Met Val Ser Ala
 4645 4650 4655
 Asn Gly Arg Trp Val Tyr Lys Leu Gln Gly Ser Thr Asn Ser Gln Gly
 4660 4665 4670
 Glu Tyr Ser Ala Ala Leu Gly Ala Gly Ile Gln Trp
 4675 4680

<210> 11
 <211> 990
 <212> PRT

<213> shigella flexneri

<400> 11

Met Thr Asn Leu Gly Glu Asp Ala Leu Lys Trp Asp Lys Asp Asn Gly
1 5 10 15
Val Phe Thr Ala Ala His Gly Thr Glu Thr Thr Ser Lys Ile Thr Asn
20 25 30
Val Lys Asp Gly Asp Leu Thr Thr Gly Ser Thr Asp Ala Val Asn Gly
35 40 45
Ser Gln Leu Lys Thr Thr Asn Asp Ala Val Ala Thr Asn Thr Thr Asn
50 55 60
Ile Ala Thr Asn Thr Thr Asn Ile Ser Asn Leu Thr Glu Thr Val Thr
65 70 75 80
Asn Leu Gly Glu Asp Ala Leu Lys Trp Asp Lys Asp Asn Gly Val Phe
85 90 95
Thr Ala Ala His Gly Asn Asn Thr Ala Ser Lys Ile Thr Asn Ile Leu
100 105 110
Asp Gly Thr Val Thr Ala Thr Ser Ser Asp Ala Ile Asn Gly Ser Gln
115 120 125
Leu Tyr Asp Leu Ser Ser Asn Ile Ala Thr Tyr Phe Gly Gly Asn Ala
130 135 140
Ser Val Asn Thr Asp Gly Val Phe Thr Gly Pro Thr Tyr Lys Ile Gly
145 150 155 160
Glu Thr Asn Tyr Tyr Asn Val Gly Asp Ala Leu Ala Ala Ile Asn Ser
165 170 175
Ser Phe Ser Thr Ser Leu Gly Asp Ala Leu Leu Trp Asp Ala Thr Ala
180 185 190
Gly Lys Phe Ser Ala Lys His Gly Thr Asn Gly Asp Ala Ser Val Ile
195 200 205
Thr Asp Val Ala Asp Gly Glu Ile Ser Asp Ser Ser Ser Asp Ala Val
210 215 220
Asn Gly Ser Gln Leu His Gly Val Ser Ser Tyr Val Val Asp Ala Leu
225 230 235 240
Gly Gly Gly Ala Glu Val Asn Ala Asp Gly Thr Ile Thr Ala Pro Thr
245 250 255
Tyr Thr Ile Ala Asn Ala Asp Tyr Asp Asn Val Gly Asp Ala Leu Asn
260 265 270
Ala Ile Asp Thr Thr Pro Asp Asp Ala Leu Leu Trp Asp Ala Asp Ala
275 280 285
Gly Glu Asn Gly Ala Phe Ser Ala Ala His Gly Lys Asp Lys Thr Ala
290 295 300
Ser Val Ile Thr Asn Val Ala Asn Gly Ala Ile Ser Ala Ala Ser Ser
305 310 315 320

Asp Ala Ile Asn Gly Ser Gln Leu Tyr Thr Thr Asn Lys Tyr Ile Ala
 325 330 335
 Asp Ala Leu Gly Gly Asp Ala Glu Val Asn Ala Asp Gly Thr Ile Thr
 340 345 350
 Ala Pro Thr Tyr Thr Ile Ala Asn Ala Glu Tyr Asn Asn Val Gly Asp
 355 360 365
 Ala Leu Asp Ala Leu Asp Asp Asn Ala Leu Leu Trp Asp Lys Thr Ala
 370 375 380
 Asn Gly Gly Ala Gly Ala Tyr Asn Ala Ser His Asp Gly Lys Ala Ser
 385 390 395 400
 Ile Ile Thr Asn Val Ala Asn Gly Ser Ile Ser Glu Asp Ser Thr Asp
 405 410 415
 Ala Val Asn Gly Ser Gln Leu Asn Ala Thr Asn Met Met Ile Glu Gln
 420 425 430
 Asn Thr Gln Ile Ile Asn Gln Leu Ala Gly Asn Thr Asp Ala Thr Tyr
 435 440 445
 Ile Glu Glu Asn Gly Ala Gly Ile Asn Tyr Val Arg Thr Asn Asp Asn
 450 455 460
 Asp Leu Ala Phe Asn Asp Ala Ser Ala Ser Gly Val Gly Ala Thr Ala
 465 470 475 480
 Val Gly Tyr Asn Ala Val Ala Ser Gly Ala Ser Ser Val Ala Ile Gly
 485 490 495
 Gln Asn Ser Ser Ser Thr Val Asp Thr Gly Ile Ala Leu Gly Ser Ser
 500 505 510
 Ser Val Ser Ser Arg Val Ile Ala Lys Gly Ser Arg Asp Thr Ser Val
 515 520 525
 Thr Glu Asn Gly Val Val Ile Gly Tyr Asp Thr Thr Asp Gly Glu Leu
 530 535 540
 Leu Gly Ala Leu Ser Ile Gly Asp Asp Gly Lys Tyr Arg Gln Ile Ile
 545 550 555 560
 Asn Val Ala Asp Gly Ser Glu Ala His Asp Ala Val Thr Val Arg Gln
 565 570 575
 Leu Gln Asn Ala Ile Gly Ala Val Ala Thr Thr Pro Thr Lys Tyr Phe
 580 585 590
 His Ala Asn Ser Thr Ala Glu Asp Ser Leu Ala Val Gly Glu Asp Ser
 595 600 605
 Leu Ala Met Gly Ala Lys Thr Val Val Asn Gly Asn Ala Gly Ile Gly
 610 615 620
 Ile Gly Leu Asn Thr Leu Val Leu Ala Asp Ala Ile Asn Gly Ile Ala
 625 630 635 640
 Ile Gly Ser Asn Ala Arg Ala Asn His Ala Asn Ser Ile Ala Met Gly
 645 650 655
 Asn Gly Ser Gln Thr Thr Arg Gly Ala Gln Thr Gly Tyr Thr Ala Tyr

660					665					670					
Asn	Met	Asp	Ala	Pro	Gln	Asn	Ser	Val	Gly	Glu	Phe	Ser	Val	Gly	Ser
		675					680					685			
Glu	Asp	Gly	Gln	Arg	Gln	Ile	Thr	Asn	Val	Ala	Ala	Gly	Ser	Ala	Asp
	690					695					700				
Thr	Asp	Ala	Val	Asn	Val	Gly	Gln	Leu	Lys	Val	Thr	Asp	Glu	Arg	Val
705					710					715					720
Ala	Gln	Asn	Thr	Gln	Ser	Ile	Thr	Asn	Leu	Asn	Asn	Gln	Val	Thr	Asn
				725					730					735	
Leu	Asp	Thr	Arg	Val	Thr	Asn	Ile	Glu	Asn	Gly	Ile	Gly	Asp	Ile	Val
			740					745					750		
Thr	Thr	Gly	Ser	Thr	Lys	Tyr	Phe	Lys	Thr	Asn	Thr	Asp	Gly	Val	Asp
		755					760					765			
Ala	Asn	Ala	Gln	Gly	Lys	Asp	Ser	Val	Ala	Ile	Gly	Ser	Gly	Ser	Ile
	770					775					780				
Ala	Ala	Ala	Asp	Asn	Ser	Val	Ala	Leu	Gly	Thr	Gly	Ser	Val	Ala	Glu
785					790					795					800
Glu	Glu	Asn	Thr	Ile	Ser	Val	Gly	Ser	Ser	Thr	Asn	Gln	Arg	Arg	Ile
				805					810					815	
Thr	Asn	Val	Ala	Ala	Ser	Val	Asn	Ala	Thr	Asp	Ala	Val	Asn	Val	Ser
			820					825					830		
Gln	Leu	Lys	Ser	Ser	Glu	Ala	Gly	Gly	Val	Arg	Tyr	Asp	Thr	Lys	Ala
		835					840					845			
Asp	Gly	Ser	Ile	Asp	Tyr	Ser	Asn	Ile	Thr	Leu	Gly	Gly	Gly	Asn	Gly
	850					855					860				
Ser	Thr	Thr	Arg	Ile	Ser	Asn	Val	Ser	Ala	Gly	Val	Asn	Asn	Asn	Asp
865					870					875					880
Ala	Val	Asn	Tyr	Ala	Gln	Leu	Lys	Gln	Ser	Ala	Gln	Glu	Thr	Lys	Gln
				885					890					895	
Tyr	Thr	Asp	Gln	Arg	Met	Val	Glu	Met	Asp	Asn	Lys	Leu	Ser	Lys	Thr
			900					905					910		
Glu	Ser	Lys	Leu	Ser	Gly	Gly	Ile	Ala	Ser	Ala	Met	Ala	Met	Thr	Gly
		915					920					925			
Leu	Pro	Gln	Ala	Tyr	Thr	Pro	Gly	Ala	Ser	Met	Ala	Ser	Ile	Gly	Gly
	930					935					940				
Gly	Thr	Tyr	Asn	Gly	Glu	Ser	Ala	Val	Ala	Leu	Gly	Val	Ser	Met	Val
945					950					955					960
Ser	Ala	Asn	Gly	Arg	Trp	Val	Tyr	Lys	Leu	Gln	Gly	Ser	Thr	Asn	Ser
				965					970					975	
Gln	Gly	Glu	Tyr	Ser	Ala	Ala	Leu	Gly	Ala	Gly	Ile	Gln	Trp		
			980					985					990		

<210> 12
 <211> 227

<212> PRT
<213> Brucella melitensis

<400> 12
Met Ser Phe Phe Lys Lys Asn Ile Ser Ile Thr Ala Met Gly Gly Leu
1 5 10 15

Met Leu Ser Leu Ala Val Asp Ala Ala Lys Ala Glu Glu Asn Val Ser
20 25 30

Gln Val Lys Leu Pro Pro Val Phe Val Phe Glu Leu Val Glu Asn Gln
35 40 45

Gly Leu Ala Asn Ile Ala Leu Ile Arg Pro Arg Val Ile Ala Pro Asp
50 55 60

Asn Asn Leu Arg Pro Gly Gly Ile Val Ser Gly Ile Ala Gly Leu Leu
65 70 75 80

Thr Leu Gly Gln Glu Asn Arg Asn Leu Ile Ser Glu Asn Arg Gln Val
85 90 95

Ile Asn Asn Asn Thr Thr Ala Ile Gly Gln Asn Arg Thr Ser Ile Ser
100 105 110

Thr Asn Ala Lys Gly Val Ala Asp Asn Arg Ala Ala Ile Arg Gln Asn
115 120 125

Ser Ala Ala Ile Ser Ala Leu Gly Gln Arg Val Asp Gly Leu Gln Gly
130 135 140

Gln Ile Asn Ser Ala Arg Lys Glu Ala Arg Ala Gly Ala Ala Asn Ala
145 150 155 160

Ala Ala Leu Ser Gly Leu Arg Tyr Asp Asn Arg Pro Gly Lys Val Ser
165 170 175

Ile Ala Thr Gly Val Gly Gly Phe Lys Gly Ser Thr Ala Leu Ala Ala
180 185 190

Gly Ile Gly Tyr Thr Ser Lys Asn Glu Asn Ala Arg Tyr Asn Val Ser
195 200 205

Val Ala Tyr Asn Glu Ala Gly Thr Ser Trp Asn Ala Gly Ala Ser Phe
210 215 220

Thr Leu Asn
225

<210> 13
<211> 311
<212> PRT
<213> Brucella suis

<400> 13
Met Ser Phe Phe Lys Lys Asn Ile Ser Ile Thr Ala Met Gly Gly Leu
1 5 10 15

Met Leu Ser Leu Ala Val Asp Ala Ala Lys Ala Glu Glu Asn Val Ser
20 25 30

Gln Val Lys Leu Pro Pro Val Phe Val Phe Glu Leu Val Glu Asn Gln
35 40 45

Gly Leu Ala Asn Ile Ala Leu Ile Arg Pro Arg Val Ile Ala Pro Asp
 50 55 60
 Asn Asn Leu Arg Pro Gly Gly Ile Val Ser Gly Ile Ala Gly Leu Leu
 65 70 75 80
 Thr Leu Gly Gln Glu Asn Arg Asn Leu Ile Ser Glu Asn Arg Gln Val
 85 90 95
 Ile Asn Asn Asn Thr Thr Ala Ile Gly Gln Asn Ser Asp Arg Ile Asp
 100 105 110
 Ala Asn Ala Lys Gly Val Ala Asp Asn Arg Ala Ala Ile Gly Gln Asn
 115 120 125
 Ser Gly Arg Ile Asp Ala Asn Ala Lys Gly Val Ala Asp Asn Lys Ala
 130 135 140
 Ala Ile Gly Arg Asn Ser Gly Arg Ile Asp Ala Asn Ala Lys Gly Val
 145 150 155 160
 Ala Asp Asn Lys Thr Ala Ile Gly Arg Asn Ser Gly Arg Ile Asp Thr
 165 170 175
 Asn Ala Lys Gly Val Ala Asp Asn Arg Ala Ala Ile Ser Gln Asn Arg
 180 185 190
 Gly Arg Ile Asn Ala Asn Ala Ala Gly Val Ala Ser Asn Arg Ala Ala
 195 200 205
 Ile Arg Gln Asn Ser Ala Ala Ile Ser Ala Leu Gly Gln Arg Val Asp
 210 215 220
 Gly Leu Gln Gly Gln Ile Asn Ser Ala Arg Lys Glu Ala Arg Ala Gly
 225 230 235 240
 Ala Ala Asn Ala Ala Ala Leu Ser Gly Leu Arg Tyr Asp Asn Arg Pro
 245 250 255
 Gly Lys Val Ser Ile Ala Thr Gly Val Gly Gly Phe Lys Gly Ser Thr
 260 265 270
 Ala Leu Ala Ala Gly Ile Gly Tyr Thr Ser Lys Asn Glu Asn Ala Arg
 275 280 285
 Tyr Asn Val Ser Val Ala Tyr Asn Glu Ala Gly Thr Ser Trp Asn Ala
 290 295 300
 Gly Ala Ser Phe Thr Leu Asn
 305 310

<210> 14
 <211> 1309
 <212> PRT
 <213> Ralstonia solanacearum

<400> 14
 Met Val Phe Ser Ala Met Pro Gln Tyr Ala Cys Ala Glu Met Leu Leu
 1 5 10 15
 Gln Asn Asp Pro Gly Thr Asn Cys Gly Ser Val Gly Asp Ala Tyr Ala
 20 25 30

Trp Ala Arg Gly Asp Gly Tyr Ser Gly Cys Lys Val Gly Tyr Glu Ala
 35 40 45
 Ala Lys Asn Leu Ala Lys Gly Thr Ala Phe Gly Asn Ser Leu Gly Gln
 50 55 60
 Leu Ser Pro Gly Thr Asn Ile Leu Val Tyr Gly Ser Thr Leu Arg Ala
 65 70 75 80
 Gly Met Asn Asp Glu Val Thr Pro Leu Asp Ser Met Asn Ile Gly Gly
 85 90 95
 His Leu Asp Val Trp Gly Ala Ser Gly Phe His Gly Gly Val Asp Met
 100 105 110
 Asn Asn Ser Ala Ile Lys Asn Leu Ala Asp Gly Thr Leu Ser Ala Thr
 115 120 125
 Ser Thr Glu Ala Val Thr Gly Arg Gln Leu Asn Ala Thr Asn Thr Asn
 130 135 140
 Ile Thr Asn Leu Gln Asn Ser Ile Lys Ser Ile Ser Ser Ser Ala Ser
 145 150 155 160
 Leu Val Gln Gln Ser Ala Ala Gly Lys Asp Ile Thr Val Ala Lys Asp
 165 170 175
 Leu Asp Gly Asp Ala Val Asp Phe Ser Gly Lys Lys Leu Ser Asp Ser
 180 185 190
 Thr Thr Phe Ser Arg Lys Leu Thr Gly Val Ala Glu Gly Thr Leu Ser
 195 200 205
 Ala Thr Ser Thr Asp Ala Val Ser Gly Lys Gln Leu Tyr Thr Thr Asn
 210 215 220
 Gln Asn Leu Ser Thr Thr Asn Gln Asn Leu Ala Asp Thr Asn Lys Ser
 225 230 235 240
 Leu Ala Glu Thr Asn Lys Asn Val Ser Ala Thr Thr Thr Asn Ile Thr
 245 250 255
 Asn Leu Gln Asn Thr Ile Lys Asn Ile Ser Gly Gly Ser Ala Gly Leu
 260 265 270
 Val Gln Gln Ser Ala Ala Gly Lys Asp Ile Thr Val Ala Lys Asp Leu
 275 280 285
 Asp Gly Glu Ala Val Asp Phe Ser Gly Lys Lys Leu Ser Asp Ser Thr
 290 295 300
 Thr Phe Ser Arg Lys Leu Thr Gly Val Ala Glu Gly Thr Leu Ser Ala
 305 310 315 320
 Thr Ser Thr Asp Ala Val Ser Gly Lys Gln Leu Tyr Thr Thr Asn Gln
 325 330 335
 Asn Leu Ala Ser Thr Asn Lys Asp Leu Ala Asn Thr Asn Thr Arg Leu
 340 345 350
 Thr Thr Ala Glu Gly Asn Leu Ser Ser Asn Thr Thr Ser Ile Thr Asn
 355 360 365

Leu Gln Asn Thr Ile Lys Asn Ile Ser Gly Gly Ser Ala Gly Leu Val
 370 375 380
 Gln Gln Ser Ala Ala Gly Lys Asp Ile Thr Val Ala Lys Asp Leu Asp
 385 390 395 400
 Gly Asp Ala Val Asp Phe Ser Gly Lys Lys Leu Ser Asp Ser Thr Thr
 405 410 415
 Phe Ser Arg Lys Leu Thr Gly Val Ala Glu Gly Thr Leu Ser Ala Thr
 420 425 430
 Ser Thr Asp Ala Val Ser Gly Arg Gln Leu Tyr Thr Thr Asn Gln Asn
 435 440 445
 Leu Ser Thr Thr Asn Gln Asn Leu Ala Asp Thr Asn Lys Ser Leu Ala
 450 455 460
 Glu Thr Asn Lys Asn Val Ser Ala Thr Thr Thr Asn Ile Thr Asn Leu
 465 470 475 480
 Gln Asn Thr Val Asn Asn Ile Ser Ser Gly Ser Ala Gly Leu Val Gln
 485 490 495
 Gln Ser Ala Ala Gly Lys Asp Ile Thr Val Ala Lys Asp Leu Asp Gly
 500 505 510
 Asp Ala Val Asp Phe Ser Gly Lys Lys Leu Ser Asp Ser Thr Thr Phe
 515 520 525
 Ser Arg Lys Leu Thr Gly Val Ala Glu Gly Thr Leu Ser Ala Thr Ser
 530 535 540
 Thr Asp Ala Val Ser Gly Lys Gln Leu Tyr Thr Thr Asn Gln Asn Leu
 545 550 555 560
 Ser Thr Thr Asn Gln Asn Leu Ala Asp Thr Asn Lys Ser Leu Ala Glu
 565 570 575
 Thr Asn Lys Asn Val Ser Ala Thr Thr Thr Asn Ile Thr Asn Leu Gln
 580 585 590
 Asn Thr Val Asn Asn Ile Ser Ser Gly Ser Ala Gly Leu Val Gln Gln
 595 600 605
 Ser Ala Ala Gly Lys Asp Ile Thr Val Ala Lys Asn Leu Asp Gly Asp
 610 615 620
 Ala Val Asp Phe Ser Gly Lys Lys Leu Ser Asp Ser Thr Thr Phe Ser
 625 630 635 640
 Arg Lys Leu Thr Gly Val Ala Glu Gly Thr Leu Ser Ala Thr Ser Thr
 645 650 655
 Asp Ala Val Ser Gly Lys Gln Leu Tyr Thr Thr Asn Gln Asn Leu Ala
 660 665 670
 Ser Thr Asn Lys Asp Leu Ala Asn Thr Asn Thr Arg Leu Thr Thr Ala
 675 680 685
 Glu Gly Asn Leu Ser Ser Asn Thr Thr Ser Ile Thr Asn Leu Gln Asn
 690 695 700
 Thr Ile Lys Asn Ile Ser Gly Gly Ser Ala Gly Leu Val Gln Gln Ser

705					710					715					720
Ala	Ala	Gly	Lys	Asp 725	Ile	Thr	Val	Ala	Lys 730	Asp	Leu	Asp	Gly	Asp 735	Ala
Val	Asp	Phe	Ser 740	Gly	Lys	Asn	Leu	Ser 745	Asp	Ser	Thr	Thr	Phe 750	Ser	Arg
Lys	Leu	Thr 755	Gly	Val	Ala	Glu	Gly 760	Thr	Leu	Ser	Ala	Thr 765	Ser	Thr	Asp
Ala	Val 770	Ser	Gly	Lys	Gln	Leu 775	Tyr	Thr	Thr	Asn	Gln 780	Asn	Leu	Ser	Thr
Thr 785	Asn	Gln	Asn	Leu	Ala 790	Asp	Thr	Asn	Lys	Ser 795	Leu	Ala	Lys	Thr	Asn 800
Asn	Asn	Val	Ser	Ala 805	Thr	Thr	Thr	Asn	Ile 810	Thr	Asn	Leu	Gln	Asn 815	Thr
Val	Asn	Asn	Ile 820	Ser	Ser	Gly	Ser	Ala 825	Gly	Leu	Val	Gln	Gln 830	Ser	Ala
Ala	Gly	Lys 835	Asp	Ile	Thr	Val	Ala 840	Lys	Asp	Leu	Asp	Gly 845	Asp	Ala	Val
Asp	Phe 850	Ser	Gly	Lys	Lys	Leu 855	Ser	Asp	Ser	Thr	Thr 860	Phe	Ser	Arg	Lys
Leu 865	Thr	Gly	Val	Ala	Glu 870	Gly	Thr	Leu	Ser	Ala 875	Thr	Ser	Thr	Asp	Ala 880
Val	Ser	Gly	Lys	Gln 885	Leu	Tyr	Ala	Thr	Asn 890	Gln	Asn	Val	Ser	Lys 895	Leu
Ser	Ala	Asn	Val 900	Thr	Asp	Val	Ser	Asp 905	Ser	Val	Thr	Asn	Ile 910	Lys	Asn
Thr	Met	Asn 915	Thr	Ile	Val	Asn	Gly 920	Gly	Gly	Leu	Lys	Tyr 925	Phe	His	Ala
Asn 930	Ser	Thr	Leu	Asp	Asp	Ala 935	Gln	Ala	Met	Gly	Leu	Glu	Ser	Ile	Ala
Phe 945	Gly	Gly	Ala	Ala	Val 950	Ala	Ala	Gly	Met	Asn 955	Ser	Met	Ala	Met	Gly 960
Gly	Asn	Ala	Arg	Ala 965	Val	Ala	Gly	Asn	Ala 970	Val	Ala	Leu	Gly	Ala 975	Gly
Ser	Val	Ala	Asp 980	Arg	Ala	Asn	Thr	Val 985	Ser	Val	Gly	Ser	Ala 990	Gly	Lys
Glu	Arg	Gln 995	Ile	Thr	Asn	Val	Ala 1000	Ala	Gly	Thr	Ala	Asp 1005	Thr	Asp	Ala
Val 1010	Asn	Val	Ala	Gln	Leu	Lys 1015	Ala	Ala	Gly	Ile	Ile 1020	Asn	Gly	Ser	Gly
Arg 1025	Thr	Asn	Ala	Thr	Val 1030	Thr	Tyr	Gly	Thr	Asn 1035	Ala	Asp	Gly	Ser	Ala 1040
Asp	Tyr	Gly	Asn	Val	Thr	Leu	Gly	Gly	Gly	Asn	Ala	Pro	Ala	Gly	Thr

1045	1050	1055
Ala Ile His Asn Val Ala Ala Gly Thr Ala Glu Thr Asp Ala Val Asn 1060	1065	1070
Val Arg Gln Met Asn Ala Ala Ile Ala Ser Val Gln Lys Val Ser Asn 1075	1080	1085
Thr Asn Asp Pro Met Phe Ala Ala Asp Gly Asp Arg Ala Val Lys Arg 1090	1095	1100
Ala Ser Ala Lys Gly Thr His Ala Thr Ala Met Gly Ala Ala Ala Ser 1105	1110	1115
Ala Gly Gly Asp Gln Ser Val Ala Thr Gly His Asn Ala Gln Ser Gly 1125	1130	1135
Gly Asp Ser Ser Val Ala Met Gly Ala Asn Ala Lys Ala Thr Ala Asn 1140	1145	1150
His Ala Val Ala Val Gly Ser Gly Ser Val Ala Asn Arg Ala Asn Thr 1155	1160	1165
Met Ser Val Gly Ser Ala Gly Ser Glu Arg Gln Ile Thr Asn Val Ala 1170	1175	1180
Ala Gly Val Gln Gly Thr Asp Ala Val Asn Val Ser Gln Leu Ser Gln 1185	1190	1195
Ala Val Tyr Ala Ala Val Gly Asp Leu Pro Ala Gly Thr Thr Ala Arg 1205	1210	1215
Gln Tyr Thr Asp Glu Gln Ile Gly Met Val Arg Gln Gly Ile Ser Gln 1220	1225	1230
Val Ala Arg Gly Ala Tyr Ser Gly Ile Ala Ala Ala Thr Ala Leu Thr 1235	1240	1245
Met Ile Pro Asp Val Asp Gln Gly Lys Ser Ile Ala Ile Gly Ile Gly 1250	1255	1260
Ser Ala Thr Tyr Lys Gly Tyr Gln Ala Val Ala Leu Gly Ala Ser Ala 1265	1270	1275
Arg Ile Ser His Asn Leu Lys Ala Lys Met Gly Val Gly Tyr Ser Ser 1285	1290	1295
Glu Gly Thr Thr Val Gly Met Gly Ala Ser Tyr Gln Trp 1300	1305	
<210> 15		
<211> 1291		
<212> PRT		
<213> Sinorhizobium meliloti		
<400> 15		
Met Ala Leu Gly Arg Gln Ser Val Ser Ala Gly Ser Gly Ser Leu Ala 1	5	10
Phe Gly Asn Gly Ser Tyr Ala Asn Ser Asn Gly Ser Val Ala Ile Gly 20	25	30
Gln Ser Ala Tyr Ala Ala Asn Val Arg Ala Ile Ala Ile Gly Gly Asp 35	40	45

Asp Ala Phe Ala Trp Arg Glu Ala Glu Gln Thr Lys Ala Gly Gly Ser
 50 55 60
 Gln Ser Ile Ala Met Gly Val Arg Ala Arg Thr Lys Ser Leu Val Val
 65 70 75 80
 Asp Asp Pro Asp Thr Val Ala Asn Glu Ala Asp Pro Gly Gly Ala Ser
 85 90 95
 Asp Ala Ile Ala Ile Gly Thr Asp Ala Gln Ala Asn Gly Asp Arg Ser
 100 105 110
 Leu Ala Ile Gly Arg Gln Asn Gln Ala Gly Asn Glu Gln Ser Ile Gly
 115 120 125
 Ile Gly Ala Gly Asn Thr Ala Thr Gly Lys Leu Ser Ile Gly Ile Gly
 130 135 140
 Ser Ser Asn Val Ala Ser Gly Glu Gln Ser Leu Ser Leu Gly Ala Gly
 145 150 155 160
 Asn Asn Ala Leu Gly Gln Gly Ser Ile Ser Ile Gly Thr Glu Thr Thr
 165 170 175
 Ala Gly Gly Leu Arg Ser Ile Ala Phe Gly Val Arg Ala Ser Thr Lys
 180 185 190
 Glu Ala Asn Leu Asp Ile Pro Asp Asp Val Ala Ala Ile Asp Ala Ile
 195 200 205
 Ala Ile Gly Thr Asn Thr Lys Ala Asn Gly Asp Arg Ser Val Ser Ile
 210 215 220
 Gly Thr Gly Ser Gln Ala Ser Ser Gly Ala Val Ser Ile Gly Asp Ala
 225 230 235 240
 Ala Lys Ala Val Gly Asp Lys Ser Val Ser Ile Gly Thr Glu Ser Trp
 245 250 255
 Ala Asp Gly Asp Glu Ser Val Ser Ile Gly Leu Val Asn Asn Ala Gly
 260 265 270
 Phe Glu Gly Asn Asp Arg Ile Lys Gly Gly Gln Thr Ser Val Ser Leu
 275 280 285
 Gly Ala Phe Asn Gln Ser Pro Gly Ile Glu Ala Ile Ala Ile Gly Ala
 290 295 300
 Arg Asn Glu Ala Asn Ala Asp Arg Ser Ile Ala Ile Gly Ser Arg Ala
 305 310 315 320
 Lys Thr Lys Ala Ala Asp Pro Ala Gln Ala Asp Gly Gly Ala Arg Asp
 325 330 335
 Ala Val Ala Ile Gly Thr Asp Ala Leu Ala Asn Asp Asp Arg Ser Ile
 340 345 350
 Ser Ile Gly Trp Asn Ser Ser Thr Ser Leu Asn Asp Ser Ile Ser Ile
 355 360 365
 Gly Thr Arg Ala Thr Ser Gly Ser Ala Gly Asp Ile Met Ile Gly Thr
 370 375 380

Gly 385 Ser Gly Thr Gly 390 Ser Thr Ser Gly Gln Asn 395 Asn Val Ala Leu Gly 400
 Val Ala Ala Ser Gln 405 Lys Val Lys Gly Ser 410 Ser Asn Ile Ala Ile Gly 415
 Asp Ser Ala Gly 420 Gly Ser Arg Glu Gly 425 Asp Asn Asn Val Ala Ile Gly 430
 Thr Asn Ala Gly 435 Ile Gln Phe Ser 440 Glu Ser Glu His Glu 445 Thr Ala Val
 Arg Ala 450 Asp Leu Val Val Ser 455 Asp Ala Val Ser Ile Gly 460 Asn Glu Ala
 Leu 465 Ala Ser Ala Asp Glu 470 Ala Ile Ala Ile Gly 475 Thr Gly Ala Val Ala 480
 Ser Gly Leu Lys Ser 485 Ile Ser Ile Gly Val 490 Gly Asn Thr Val Ser Gly 495
 Ala Ser Ser Gly 500 Ala Ile Gly Asp Pro 505 Thr Asp Ile Thr Gly 510 Thr Gly
 Ser Tyr Ser 515 Leu Gly Asn Asp Asn 520 Thr Ile Ala Ala Asp 525 Asn Ala Gly
 Thr Phe Gly 530 Asn Asp Asn Thr 535 Leu Ala Asp Ala Ala 540 Asp Gly Ser Arg
 Val 545 Ile Gly Asn Gly Asn 550 Asn Ile Asp Val Ser 555 Asp Ala Phe Val Leu 560
 Gly Asn Gly Ala Asp 565 Val Thr Glu Val Gly 570 Gly Val Ala Leu Gly 575 Ser
 Gly Ser Val Ser 580 Asp Thr Gly Ala Asp 585 Val Ala Gly Tyr Val 590 Pro Gly
 Gly Ala Ser 595 Thr Ala Asp Gln Asn 600 Ala Ile Glu Ala Thr 605 Gln Ser Thr
 Arg Gly 610 Ala Val Ala Val Gly 615 Asn Pro Asp Ala Glu 620 Thr Gly Val Tyr
 Arg Gln 625 Ile Thr Gly Val 630 Ala Ala Gly Thr Ala 635 Asp Ser Asp Ala Ala 640
 Asn Val Ala Gln 645 Leu Lys Ser Val Glu 650 Thr Ile Ala Lys Thr Gly 655 Trp
 Lys Leu Thr Thr 660 Asp Ser Gly Ser Ile 665 Asp Gly Ile Gly Pro 670 Gly Asp
 Glu Leu Val 675 Leu Lys Gly Gly Asp 680 Gly Asn Ile Val Ile 685 Ser Asn Gln
 Ile Leu 690 Ser Asn Asp Val Ser 695 Ile Asp Leu Ala Asp 700 Glu Ile Glu Val
 Asn Arg Val 705 Thr Ala Arg 710 Asp Pro Asp Thr Gly 715 Ala Ser Thr Val Leu 720

Asp Glu Asn Gly Leu Ser Phe Thr Thr Gln Asp Ala Asn Gly Glu Asp
 725 730 735
 Thr Ala Leu Gly Pro Arg Val Thr Ala Ala Gly Ile Gln Ala Ala Gly
 740 745 750
 Lys Ile Thr Asn Val Ala Ala Gly Glu Ala Asp Thr Asp Ala Val Asn
 755 760 765
 Phe Ser Gln Leu Arg Gln Val Glu Thr Ala Ser Gly Asn Thr Asp Gln
 770 775 780
 Arg Ala Val Lys Tyr Asp Trp Thr Asp Ala Asn Thr Asn Gly Val Ile
 785 790 795 800
 Asp Glu Gly Glu Leu Asn Leu Asp Ser Val Thr Leu Ala Gly Gly Met
 805 810 815
 Gly Gly Thr Arg Ile Ser Asn Leu Ala Pro Gly Ala Leu Ser Ala Ala
 820 825 830
 Ser Thr Asp Ala Val Asn Gly Ser Gln Leu Phe Gly Leu Arg Ser Arg
 835 840 845
 Val Ser Asn Val Ala Val Ala Leu Gly Gly Gly Ala Ala Tyr Asp Pro
 850 855 860
 Val Lys Asp Glu Trp Ile Ala Pro Lys Tyr Thr Ile Gly Gly Thr Asp
 865 870 875 880
 Tyr Ser Asn Val Gly Asp Ala Leu Ala Ala Val Gly Gly Thr Ala Gly
 885 890 895
 Ala Gly Trp Ser Leu Ser Ala Gln Gly Ala Asn Ala Ser Asn Val Ala
 900 905 910
 Pro Gly Glu Thr Val Asp Leu Arg Ser Gly Asp Gly Asn Ile Val Val
 915 920 925
 Ser Lys Ala Glu Thr Gly Asp Thr Val Ser Phe Asp Leu Ala Asp Asp
 930 935 940
 Leu Asp Val Ser Glu Ser Ile Thr Val Gly Ala Asp Pro Ala Asp Pro
 945 950 955 960
 Asn Ala Pro Thr Thr Val Ile Thr Gly Gly Ser Ile Val Ile Gly Ser
 965 970 975
 Thr Met Leu Gly Ser Asn Gly Leu Val Ile Thr Gly Gly Pro Ser Val
 980 985 990
 Thr Thr Asp Gly Ile Asp Ala Gly Gly Met Lys Val Thr Asn Val Ala
 995 1000 1005
 Asn Gly Thr Val Ala Lys Asp Ser Lys Asp Ala Val Asn Gly Gly Gln
 1010 1015 1020
 Leu Phe Asp Val Val Ala Asn Ala Thr Ala Asn Gly Val Gly Tyr Asp
 1025 1030 1035 1040
 Asp Lys Ser Lys Gly Thr Leu Thr Leu Glu Gly Ala Asn Gly Thr Lys
 1045 1050 1055

Ile Thr Asn Val Ala Ala Gly Asp Leu Asn Ala Asn Ser Thr Asp Ala
 1060 1065 1070
 Val Asn Gly Ser Gln Leu Tyr Ala Thr Asn Val Lys Val Asp Arg Leu
 1075 1080 1085
 Asp Thr Glu Val Lys Glu Ile Asp Ser Arg Val Thr Tyr Ile Glu Ser
 1090 1095 1100
 Phe Gln Gly Asp Leu Glu Asn Ala Ala Val Tyr Asp Thr Asp Ala Ala
 1105 1110 1115 1120
 Gly Lys Arg Leu Asn Thr Leu Thr Leu Glu Gly Gly Asp Pro Asp Lys
 1125 1130 1135
 Pro Val Leu Ile Ala Asn Val Ala Lys Gly Val Lys Ala Thr Asp Ala
 1140 1145 1150
 Val Asn Val Gly Gln Leu Asp Glu Ser Val Ala Glu Ser Lys Ser Tyr
 1155 1160 1165
 Thr Asp Glu Lys Thr Glu Trp Ala Ile Asp Gln Ala Ala Ile Tyr Thr
 1170 1175 1180
 Asp Gln Val Ile Glu Thr Lys Val Ser Ala Val Asn Asn Tyr Ala Gln
 1185 1190 1195 1200
 Gln Arg Phe Ala Gln Leu Ser Gly Glu Ile Gly Gln Val Arg Ser Glu
 1205 1210 1215
 Ala Arg Gln Ala Ala Ala Ile Gly Leu Ala Ala Ala Ser Leu Arg Phe
 1220 1225 1230
 Asp Asn Glu Pro Gly Lys Leu Ser Val Ala Leu Gly Gly Gly Phe Trp
 1235 1240 1245
 Arg Ser Glu Gly Ala Leu Ala Phe Gly Ala Gly Tyr Thr Ser Glu Asp
 1250 1255 1260
 Gly Arg Val Arg Ala Asn Leu Thr Gly Ala Ala Ala Gly Gly Asn Val
 1265 1270 1275 1280
 Gly Val Gly Ala Gly Leu Ser Ile Thr Leu Asn
 1285 1290

<210> 16
 <211> 372
 <212> PRT
 <213> Bradorhizobium japonicum

<400> 16
 Met Arg Ala Phe Gly Ser Gly Asn Ala Ile Asn Gly Thr Asn Tyr Ala
 1 5 10 15
 Ala Val Gly Ser Asn Asn Val Val Ala Gly Asn Asn Gly Ala Val Val
 20 25 30
 Gly Ser Gly Asn Gly Val Thr Gly Asp Asn Thr Ala Ala Phe Gly Ser
 35 40 45
 Ser Ile Gly Ile Ala Gly Gly Asn Asn Ala Ala Val Gly Ser Phe Ser
 50 55 60
 Thr Val Thr Gly Ser Asn Ser Ala Ala Val Gly Ser Phe Asn Asn Val

65					70						75					80
Ser	Gly	Asn	Asn	Ser	Gly	Ala	Phe	Gly	Thr	Gly	Gln	Asn	Ile	Arg	Gly	
				85					90					95		
Asn	Gly	Thr	Phe	Ala	Ile	Gly	Asp	Pro	Asn	Ile	Val	Asn	Gly	Asn	Asn	
			100					105					110			
Ser	Leu	Val	Phe	Gly	Asp	Asn	Asn	Thr	Val	Asn	Gly	Ser	Asn	Val	Ala	
		115					120					125				
Gly	Arg	Gly	Asp	Asn	Ile	Gln	Leu	Val	Gly	Ser	Asn	Asn	Thr	Ile	Ala	
	130					135					140					
Ala	Thr	Ser	Ser	Ala	Ala	Gly	Ser	Ser	Val	Phe	Gly	Ser	Gly	Asn	Thr	
145					150					155					160	
Val	Asn	Ala	Thr	Asn	Ala	Val	Val	Met	Gly	Asn	Asn	Ser	Thr	Val	Ser	
				165					170					175		
Gly	Ala	Ser	Ser	Val	Ala	Ile	Gly	Asn	Gly	Thr	Ala	Val	Thr	Gly	Ile	
			180					185					190			
Asn	Ala	Ile	Ala	Met	Gly	Thr	Gly	Ala	Gly	Ala	Asn	Phe	Asp	Asn	Ser	
		195					200					205				
Val	Ala	Ile	Gly	Ser	Gly	Ala	Thr	Thr	Thr	Arg	Ala	Asn	Gln	Val	Ala	
	210					215					220					
Val	Gly	Thr	Ala	Ser	Ser	Thr	Tyr	Thr	Met	Ser	Gly	Ile	Thr	Ser	Ala	
225					230					235					240	
Ala	Ser	Lys	Ala	Ala	Gln	Ser	Gly	Pro	Thr	Gln	Leu	Val	Thr	Ser	Asp	
				245					250					255		
Ala	Ala	Gly	Asn	Leu	Ala	Thr	Thr	Ser	Leu	Ala	Gly	Leu	Gly	Leu	Ala	
			260					265					270			
Ser	Ala	Gly	Asp	Ile	Asn	Gly	Ile	Asn	Ser	Gln	Leu	Ala	Ala	Leu	Asn	
		275					280					285				
Gly	Arg	Val	Asp	Asn	Leu	Thr	Arg	Glu	Ser	Arg	Gly	Gly	Val	Ala	Leu	
	290					295					300					
Ala	Leu	Ala	Ala	Ser	Ser	Leu	Gln	Phe	Asp	Pro	Arg	Pro	Gly	Lys	Ile	
305					310					315					320	
Ser	Val	Ser	Gly	Gly	Phe	Gly	Asn	Phe	Gln	Gly	Gln	Ser	Gly	Leu	Ala	
				325					330					335		
Val	Gly	Leu	Gly	Tyr	Ser	Tyr	Ser	Asp	Ala	Met	Arg	Phe	Asn	Ala	Ala	
			340					345					350			
Phe	Thr	Ala	Ala	Gln	Gln	Gly	Ala	Ile	Gly	Val	Arg	Ala	Gly	Ala	Ser	
		355					360					365				
Trp	Thr	Leu	Asn													
	370															

<210> 17
 <211> 3399
 <212> PRT
 <213> Burkholderia fungorum

<220>
 <221> Xaa
 <222> 787
 <223> Xaa is any amino acid

<400> 17

Met	Asn	Lys	Thr	Tyr	Arg	Ser	Val	Trp	Asn	Glu	Ser	Thr	Gly	Thr	Trp
1				5					10					15	
Val	Ala	Ala	Ser	Glu	His	Ala	Ser	Ala	Arg	Gly	Lys	Lys	Ser	Ser	Ala
			20					25					30		
Lys	Thr	Ser	Ser	Thr	Lys	Ala	Val	Val	Gly	Ala	Leu	Gly	Leu	Ala	Ala
		35					40					45			
Gly	Leu	Tyr	Gly	Ala	Asp	Ala	Phe	Ala	Leu	Gly	Gly	Gly	Leu	Thr	Leu
	50					55					60				
Cys	Pro	Thr	Thr	Glu	Gly	Ser	Ala	Gly	Tyr	Thr	Ala	Gly	Ser	Ala	Ser
65					70					75					80
Ser	Ala	Asn	Gly	Ala	Tyr	Cys	Gly	Ser	Asp	Tyr	Gln	Trp	Gly	Leu	Phe
				85					90					95	
Ser	Asn	Thr	Asn	Ala	Asp	Gly	Ser	Lys	Ser	Gly	Gln	Pro	Ile	Gly	Ala
			100					105					110		
Ala	Ile	Glu	Gly	Met	Asn	Asp	Gly	Ser	Leu	Leu	Leu	Tyr	Gly	Pro	Asn
		115					120					125			
Asn	Ile	Val	Met	Lys	Asn	Leu	Val	Ser	Met	Ser	Ser	Asn	Lys	Ile	Ile
	130					135					140				
Asn	Leu	Ala	Pro	Gly	Thr	Val	Ser	Ser	Thr	Ser	Ala	Asp	Ala	Val	Asn
145					150					155					160
Gly	Ser	Gln	Leu	Tyr	Ala	Thr	Asn	Gln	Asn	Val	Ser	Asn	Ile	Gly	Asn
			165					170						175	
Thr	Val	Asn	Asn	Ile	Thr	Thr	Gly	Ala	Gly	Ile	Met	Tyr	Phe	His	Val
			180					185					190		
Asn	Ser	Thr	Leu	Ala	Asp	Ser	Thr	Ala	Asn	Gly	Val	Asn	Ser	Ile	Ala
		195					200					205			
Ile	Gly	Gly	Ala	Thr	Arg	Thr	Asp	Ala	Asn	Asn	Ser	Ile	Ser	Ile	Gly
	210					215					220				
Thr	Gly	Leu	Thr	Gln	Ala	Ser	Ser	Asn	Thr	Gly	Ala	Ile	Ala	Ile	Gly
225					230					235					240
Gln	Asn	Ala	Ser	Ile	Asn	Val	Tyr	Gly	Ala	Asn	Ser	Ile	Ala	Ile	Gly
				245					250					255	
Thr	Asn	Ser	Ala	Thr	Gly	Gly	Ile	Gly	Gly	Ala	Ile	Ala	Leu	Gly	Glu
			260					265					270		
Asn	Ala	Phe	Ala	Thr	Gly	Gly	Lys	Met	Leu	Ala	Leu	Gly	Ser	Gly	Ala
		275					280					285			
Ser	Ala	Thr	Thr	Ala	Asn	Ser	Val	Ala	Leu	Gly	Ser	Gly	Ser	Thr	Thr
	290					295					300				

Thr 305	Ala	Asn	Leu	Thr	Ala 310	Ala	Gly	Tyr	Asn	Pro 315	Gly	Ser	Gly	Thr	Leu 320
Ala	Gly	Thr	Ser	Gln 325	Ala	Thr	Asn	Gly	Glu 330	Val	Ser	Val	Gly	Asn 335	Ala
Gly	Ala	Glu	Arg 340	Arg	Ile	Thr	Asn	Val 345	Ala	Ala	Gly	Ser	Ala 350	Ala	Thr
Asp	Ala	Val 355	Asn	Val	Ser	Gln	Leu 360	Gln	Ser	Glu	Asp	Ala 365	Lys	Val	Asn
Thr	Ile 370	Asn	Asn	Asn	Val	Asn 375	Asn	Leu	Ser	Gly	Ser 380	Val	Thr	Asn	Ile
Ser 385	Ser	Thr	Val	Asn	Asn 390	Ile	Thr	Asn	Gly	Gly 395	Gly	Ile	Lys	Tyr	Phe 400
His	Ala	Asn	Ser	Thr 405	Gln	Ala	Asp	Ser	Ser 410	Ala	Thr	Gly	Thr	Asp 415	Ala
Val	Ala	Ile	Gly 420	Gly	Asn	Ala	Gln	Ala 425	Thr	Ala	Ala	Asn	Ser 430	Val	Ala
Leu	Gly	Leu 435	Asn	Ser	Thr	Ser	Lys 440	Gly	Thr	Asn	Ala	Ile 445	Ala	Leu	Gly
Gly	Ala 450	Val	Ala	Gly	Gly	Ser 455	Tyr	Ala	Phe	Ala	Ala 460	Gly	Ser	Leu	Ala
Leu 465	Ala	Ala	Thr	Thr	Gly 470	Asp	Ile	Ala	Leu	Gly 475	Ser	Ser	Ala	Thr	Ala 480
Ser	Ser	Ala	Asn	Ser 485	Asn	Ala	Tyr	Ala	Thr 490	Ala	Leu	Gly	Thr	Asn 495	Ala
Leu	Ala	Asn	Ala 500	Thr	Asp	Ala	Thr	Ala 505	Ile	Gly	Glu	Gly	Ala 510	Ser	Ala
Thr	Ala	Ala 515	Ser	Ser	Val	Ala	Leu 520	Gly	Ala	Arg	Ser	Lys 525	Thr	Thr	Ala
Asn	Leu 530	Ser	Thr	Ala	Gly	Tyr 535	Asn	Pro	Gly	Thr	Gly 540	Thr	Leu	Ser	Gly
Thr 545	Thr	Pro	Thr	Gly	Glu 550	Val	Ser	Val	Gly	Ser 555	Ala	Gly	Lys	Glu	Arg 560
Arg	Val	Thr	Asn	Val 565	Ala	Ala	Gly	Ser	Ala 570	Ala	Thr	Asp	Ala	Val 575	Asn
Val	Ser	Gln	Leu 580	Met	Ser	Glu	Asp	Ala 585	Lys	Val	Asn	Thr	Ile 590	Asn	Asn
Asn	Val	Asn 595	Asn	Leu	Ser	Asn	Asn 600	Val	Thr	Asn	Ile	Ala 605	Gly	Asn	Val
Thr	Asn 610	Ile	Ser	Asn	Thr	Val 615	Asn	Asn	Ile	Thr	Asn 620	Gly	Gly	Gly	Ile
Lys 625	Tyr	Phe	His	Val	Asn 630	Ser	Thr	Leu	Ala	Asp 635	Ser	Ser	Ala	Gly	Gly 640

Thr Asn Ser Ile Ala Ile Gly Gly Gly Ala Thr Thr Gly Asn Val Thr
 645 650 655
 Ala Gly Thr Ser Asp Asn Ile Ser Ile Gly Thr Asn Ala Thr Thr Asn
 660 665 670
 Tyr Gly Lys Asn Ile Ala Ile Gly Gly Asn Ala Gln Ala Leu Gly Gly
 675 680 685
 Ala Tyr Asp Gly Gly Tyr Asn Thr Ala Ile Gly Glu Asn Ala Ile Ala
 690 695 700
 Lys Gly Asp Gly Ala Gly Gly Phe Gly Gly Gly Trp Gly Gln Thr
 705 710 715 720
 Thr Ala Ile Gly Gly Gly Ser Gln Ala Leu His Asp Asn Thr Thr Ala
 725 730 735
 Val Gly Ser Gly Ala Ile Ala Asn Val Ala Asn Ala Thr Ala Leu Gly
 740 745 750
 Met Ser Ala Ser Ala Thr Ala Gly Ser Ala Ile Ala Leu Gly Gln Gly
 755 760 765
 Ala Val Ala Ser Ala Ala Asn Ser Val Ala Leu Gly Ser Gly Ser Thr
 770 775 780
 Thr Thr Xaa Asn Leu Ser Ala Ala Gly Tyr Asn Pro Gly Thr Gly Thr
 785 790 795 800
 Leu Ser Gly Ile Ala Ser Val Ala Asn Gly Glu Val Ser Val Gly Ala
 805 810 815
 Ala Gly Lys Glu Arg Arg Ile Thr Asn Val Ala Ala Gly Ser Ala Ala
 820 825 830
 Thr Asp Ala Val Asn Val Ser Gln Leu Gln Ser Glu Asp Ala Lys Val
 835 840 845
 Asn Thr Ile Asn Asn Asn Val Asn Asn Leu Ser Gly Ser Val Thr Asn
 850 855 860
 Ile Ser Asn Thr Val Asn Asn Ile Thr Asn Gly Gly Gly Ile Lys Tyr
 865 870 875 880
 Phe His Thr Lys Ser Thr Leu Ala Asp Ser Ser Ala Thr Gly Thr Asp
 885 890 895
 Ala Val Ala Ile Gly Gly Asn Ala Gln Ala Thr Ala Ala Asn Ser Val
 900 905 910
 Ala Leu Gly Ser Asn Ser Thr Thr Thr Ala Asn Leu Ser Ala Ala Gly
 915 920 925
 Tyr Asn Pro Gly Thr Gly Ala Leu Ser Gly Ile Ala Ser Ala Ala Asn
 930 935 940
 Gly Glu Val Ser Val Gly Ala Ala Gly Lys Glu Arg Arg Ile Thr Asn
 945 950 955 960
 Val Ala Ala Gly Ser Ala Ala Thr Asp Ala Val Asn Val Ser Gln Leu
 965 970 975
 Gln Ser Glu Asp Ala Lys Val Asn Thr Ile Ser Asn Asn Val Asn Asn

980					985					990					
Leu	Ser	Gly	Ser	Val	Thr	Asn	Ile	Ser	Ser	Thr	Val	Asn	Asn	Ile	Thr
		995					1000					1005			
Asn	Gly	Gly	Gly	Ile	Lys	Tyr	Phe	His	Thr	Asn	Ser	Thr	Leu	Ala	Asp
	1010					1015					1020				
Ser	Thr	Ala	Asn	Gly	Val	Asn	Ser	Ile	Ala	Ile	Gly	Gly	Ala	Thr	Arg
	1025					1030					1035				1040
Thr	Asp	Ala	Asn	Asn	Ser	Ile	Ser	Ile	Gly	Thr	Gly	Leu	Thr	Gln	Ala
				1045					1050					1055	
Ser	Ser	Asn	Thr	Gly	Ala	Ile	Ala	Ile	Gly	Gln	Asn	Ala	Ser	Ile	Asn
			1060					1065					1070		
Val	Tyr	Gly	Ala	Asn	Ser	Ile	Ala	Ile	Gly	Thr	Asn	Ser	Ala	Thr	Gly
		1075					1080					1085			
Gly	Ile	Gly	Gly	Ala	Ile	Ala	Leu	Gly	Glu	Asn	Ala	Phe	Ala	Thr	Gly
	1090					1095					1100				
Gly	Lys	Met	Leu	Ala	Leu	Gly	Ser	Gly	Ala	Ser	Ala	Thr	Thr	Ala	Asn
	1105					1110					1115				1120
Ser	Val	Ala	Leu	Gly	Ser	Gly	Ser	Thr	Thr	Thr	Ala	Asn	Leu	Thr	Ala
				1125					1130					1135	
Ala	Gly	Tyr	Asn	Pro	Gly	Ser	Gly	Thr	Leu	Ala	Gly	Thr	Ser	Gln	Ala
				1140				1145						1150	
Thr	Asn	Gly	Glu	Val	Ser	Val	Gly	Asn	Ala	Gly	Ala	Glu	Arg	Arg	Ile
		1155					1160					1165			
Thr	Asn	Val	Ala	Ala	Gly	Ser	Ala	Ala	Thr	Asp	Ala	Val	Asn	Val	Ser
		1170					1175				1180				
Gln	Leu	Gln	Ser	Glu	Asp	Ala	Lys	Val	Asn	Thr	Ile	Asn	Asn	Asn	Val
	1185					1190					1195				1200
Asn	Asn	Leu	Ser	Asn	Asn	Val	Thr	Asn	Ile	Ala	Gly	Asn	Val	Thr	Asn
				1205					1210					1215	
Ile	Ser	Asn	Thr	Val	Asn	Asn	Ile	Thr	Asn	Gly	Gly	Gly	Ile	Lys	Tyr
			1220					1225					1230		
Phe	His	Thr	Lys	Ser	Thr	Leu	Ala	Asp	Ser	Ser	Ala	Thr	Gly	Thr	Asp
		1235					1240					1245			
Ala	Val	Ala	Ile	Gly	Gly	Asn	Ala	Gln	Ala	Thr	Ala	Ala	Asn	Ser	Val
		1250				1255					1260				
Ala	Leu	Gly	Ser	Asn	Ser	Thr	Thr	Thr	Ala	Asn	Leu	Ser	Ala	Ala	Gly
	1265					1270					1275				1280
Tyr	Asn	Pro	Gly	Thr	Gly	Thr	Leu	Ser	Gly	Thr	Thr	Pro	Thr	Gly	Glu
				1285					1290					1295	
Val	Ser	Val	Gly	Ser	Ala	Gly	Lys	Glu	Arg	Arg	Val	Thr	Asn	Val	Ala
			1300					1305					1310		
Ala	Gly	Ser	Ala	Ala	Thr	Asp	Ala	Val	Asn	Val	Ser	Gln	Leu	Gln	Ser
		1315					1320					1325			

Ala Ile Ile Gly Ser Thr Ala Asn Ala Val Ala Tyr Asp Asp Gly Thr
 1330 1335 1340

Lys Ala Thr Val Thr Leu Lys Gly Ala Ser Gly Thr Lys Ile Thr Asn
 1345 1350 1355 1360

Leu Thr Ala Gly Asn Leu Ser Ala Thr Ser Thr Asp Ala Val Asn Gly
 1365 1370 1375

Ser Gln Leu Tyr Ala Thr Asn Gln Asn Val Ser Asn Ile Gly Asn Thr
 1380 1385 1390

Val Asn Asn Ile Thr Asn Gly Gly Gly Ile Lys Tyr Phe His Ala Asn
 1395 1400 1405

Ser Thr Gln Ala Asp Ser Ser Ala Thr Gly Ser Asn Ser Val Ala Val
 1410 1415 1420

Gly Asp Arg Ala Ser Ser Leu Gly Gly Ser Ser Val Ala Met Gly Asp
 1425 1430 1435 1440

Gly Ala Thr Ala Val Gly Ala Ala Ser Ile Ala Ile Gly Asn Asn Ala
 1445 1450 1455

Gln Asn Val Thr Gly Ser Asn Asn Ser Val Ala Ile Gly Gly Asp Ser
 1460 1465 1470

Lys Ala Gly Asp Arg Ser Val Ser Leu Gly Asn Gly Ala Asp Thr Ser
 1475 1480 1485

Leu Ser Ser Trp Gly Val Ala Val Gly Thr Asn Ala Asn Val Ser Ala
 1490 1495 1500

Ala Leu Gly Thr Ala Ile Gly Ala Gly Ala Asn Val Ser Gly Ala Asn
 1505 1510 1515 1520

Ser Thr Ala Ile Gly Ala Asn Ala Val Ala Ser Ala Thr Asn Ser Val
 1525 1530 1535

Ala Leu Gly Ser Asn Ser Thr Thr Thr Ala Asn Leu Ser Ala Ala Gly
 1540 1545 1550

Tyr Asn Pro Gly Thr Gly Thr Leu Ser Gly Ile Ala Ser Ala Ala Asn
 1555 1560 1565

Gly Glu Val Ser Val Gly Ala Ala Gly Lys Glu Arg Arg Val Thr Asn
 1570 1575 1580

Val Ala Ala Gly Ser Ala Ala Thr Asp Ala Val Asn Val Ser Gln Leu
 1585 1590 1595 1600

Gln Ser Glu Asp Ala Lys Val Asn Thr Ile Asn Asn Asn Val Asn Asn
 1605 1610 1615

Leu Ser Gly Ser Val Thr Asn Ile Ser Ser Thr Val Asn Asn Ile Thr
 1620 1625 1630

Asn Gly Ser Gly Ile Lys Tyr Phe His Thr Asn Ser Thr Leu Ala Asp
 1635 1640 1645

Ser Ser Ala Gly Gly Ala Asn Ser Ile Ala Ile Gly Gly Gly Ala Ala
 1650 1655 1660

Thr Ser Ser Ser Ala Gly Leu Ser Asp Asn Met Ala Ile Gly Thr Asn
 1665 1670 1675 1680
 Ala Thr Ala Ser Tyr Gly Lys Asn Ile Ala Ile Gly Gly Gly Ala Gln
 1685 1690 1695
 Ala Thr Gly Gly Thr Tyr Asp Gly Gly Tyr Asn Val Ala Leu Gly Glu
 1700 1705 1710
 Asn Ala Asn Ala Thr Ala Gly Thr Asn Ala Trp Gly His Asn Thr Ala
 1715 1720 1725
 Ile Gly Ala Asn Thr Val Ile Asn Gly Val Asn Ser Val Ala Leu Gly
 1730 1735 1740
 Ile Ser Ala Thr Thr Ser Gly Ser Gly Ser Met Ala Phe Gly Ser Ala
 1745 1750 1755 1760
 Ala Gln Ala Ser Ala Asp Tyr Ala Ile Ala Ser Gly Ala Gly Ala Asn
 1765 1770 1775
 Ala Ser Ala Val Asn Ser Val Ala Leu Gly Ser Asn Ser Thr Thr Thr
 1780 1785 1790
 Ala Asn Leu Ser Ala Ala Gly Tyr Asn Pro Gly Thr Gly Thr Leu Ser
 1795 1800 1805
 Gly Ile Ala Ser Val Ala Asn Gly Glu Val Ser Val Gly Ser Ala Gly
 1810 1815 1820
 Lys Glu Arg Arg Val Thr Asn Val Ala Ala Gly Ser Ala Ala Thr Asp
 1825 1830 1835 1840
 Ala Val Asn Val Ser Gln Leu Gln Ser Glu Asp Ala Lys Val Asn Thr
 1845 1850 1855
 Ile Asn Asn Asn Val Asn Asn Leu Ser Asn Asn Val Ser Asn Ile Ala
 1860 1865 1870
 Gly Asn Val Thr Asn Ile Ser Asn Thr Val Asn Asn Ile Thr Asn Gly
 1875 1880 1885
 Gly Gly Gly Ile Lys Tyr Phe His Ala Asn Ser Thr Leu Ala Asp Ser
 1890 1895 1900
 Ser Ala Thr Gly Thr Asp Ala Val Ala Ile Gly Gly Asn Ala Gln Ala
 1905 1910 1915 1920
 Thr Ala Ala Asn Ser Val Ala Leu Gly Ser Asn Ser Thr Thr Thr Ala
 1925 1930 1935
 Asn Leu Ser Ala Ala Gly Tyr Asn Pro Gly Thr Gly Thr Leu Ser Gly
 1940 1945 1950
 Thr Thr Pro Val Gly Glu Val Ser Val Gly Ser Ala Gly Lys Glu Arg
 1955 1960 1965
 Arg Val Thr Asn Val Ala Ala Gly Ser Ala Ala Thr Asp Ala Val Asn
 1970 1975 1980
 Val Ser Gln Leu Gln Ser Ala Ile Ile Gly Ser Thr Ala Asn Ala Val
 1985 1990 1995 2000

Ala Tyr Asp Asp Gly Thr Lys Ala Thr Val Thr Leu Lys Gly Ala Ser
 2005 2010 2015
 Gly Thr Lys Ile Thr Asn Leu Thr Ala Gly Asn Leu Ser Ala Thr Ser
 2020 2025 2030
 Thr Asp Ala Val Asn Gly Ser Gln Leu Tyr Ala Thr Asn Gln Asn Val
 2035 2040 2045
 Ser Asn Val Gly Asn Thr Val Ser Asn Leu Ser Asn Asn Val Thr Asn
 2050 2055 2060
 Ile Ala Gly Asn Val Thr Asn Ile Ser Asn Thr Val Asn Asn Ile Thr
 2065 2070 2075 2080
 Asn Gly Gly Gly Ile Lys Tyr Phe His Ala Asn Ser Thr Leu Ala Asp
 2085 2090 2095
 Ser Ser Ala Thr Gly Thr Asp Ala Val Ala Ile Gly Gly Asn Ala Gln
 2100 2105 2110
 Ala Thr Ala Ala Asn Ser Val Ala Leu Gly Ser Asn Ser Thr Thr Thr
 2115 2120 2125
 Ala Asn Leu Ser Ala Ala Gly Tyr Asn Pro Gly Thr Gly Ala Leu Ser
 2130 2135 2140
 Ala Thr Thr Pro Val Gly Glu Val Ser Val Gly Ser Ala Gly Lys Glu
 2145 2150 2155 2160
 Arg Arg Val Thr Asn Val Ala Ala Gly Ser Ala Ala Thr Asp Ala Val
 2165 2170 2175
 Asn Val Ser Gln Leu Met Ser Glu Asp Ala Lys Val Asn Thr Ile Asn
 2180 2185 2190
 Asn Asn Val Asn Asn Leu Ser Asn Asn Val Ser Asn Ile Ala Gly Asn
 2195 2200 2205
 Val Thr Asn Ile Ser Asn Thr Val Asn Asn Ile Thr Asn Gly Gly Ser
 2210 2215 2220
 Gly Ile Lys Tyr Phe His Ala Asn Ser Thr Leu Ala Asp Ser Ser Ala
 2225 2230 2235 2240
 Thr Gly Val Asp Ala Val Ala Ile Gly Gly Asn Ala Gln Ala Thr Ala
 2245 2250 2255
 Ala Asn Ser Val Ala Leu Gly Ser Asn Ser Thr Thr Thr Ala Asn Leu
 2260 2265 2270
 Ser Ala Ala Gly Tyr Asn Pro Gly Thr Gly Ala Leu Ser Gly Ile Ala
 2275 2280 2285
 Ser Ala Ala Asn Gly Glu Val Ser Val Gly Ala Ala Gly Lys Glu Arg
 2290 2295 2300
 Arg Ile Thr Asn Val Ala Ala Gly Ser Ala Ala Thr Asp Ala Val Asn
 2305 2310 2315 2320
 Val Ser Gln Leu Gln Ser Glu Asp Ala Lys Val Asn Thr Ile Asn Asn
 2325 2330 2335

Asn Val Asn Asn Leu Ser Asn Asn Val Ser Asn Ile Ala Gly Asn Val
 2340 2345 2350
 Thr Asn Ile Ser Asn Thr Val Asn Asn Ile Thr Asn Gly Gly Ser Gly
 2355 2360 2365
 Ile Lys Tyr Phe His Ala Asn Ser Thr Leu Ala Asp Ser Ser Ala Thr
 2370 2375 2380
 Gly Thr Asp Ala Val Ala Ile Gly Gly Asn Ala Ser Ala Ser Ala Ala
 2385 2390 2395 2400
 Asn Ser Val Ala Leu Gly Ser Asn Ser Thr Thr Thr Ala Asn Leu Ser
 2405 2410 2415
 Ala Ala Gly Tyr Asn Pro Gly Ser Ala Ala Leu Ser Gly Thr Ala Ser
 2420 2425 2430
 Ala Ala Asn Gly Glu Val Ser Val Gly Ala Ala Gly Lys Glu Arg Arg
 2435 2440 2445
 Ile Thr Asn Val Ala Ala Gly Ser Ala Ala Thr Asp Ala Val Asn Val
 2450 2455 2460
 Ser Gln Leu Gln Ser Glu Asp Ala Lys Val Asn Ala Glu Gly Ala Ala
 2465 2470 2475 2480
 Thr Ala Ala Ala Leu Gly Gly Gly Ser Thr Tyr Asn Thr Thr Thr Gly
 2485 2490 2495
 Ala Ile Thr Ser Pro Thr Tyr Ile Ala Gly Gly Lys Thr Phe Asn Asn
 2500 2505 2510
 Val Gly Asp Val Val Thr Asn Ile Asp Gly Arg Val Thr Gln Asn Ser
 2515 2520 2525
 Thr Asp Ile Thr Asn Leu Thr Thr Thr Ile Asp Asn Gly Thr Ile Gly
 2530 2535 2540
 Leu Val Gln Gln Ala Thr Pro Thr Ser Thr Ile Thr Val Ala Lys Asp
 2545 2550 2555 2560
 Thr Gly Gly Ala Thr Val Asp Phe Arg Gly Thr Gly Asn Ala Thr Arg
 2565 2570 2575
 Thr Leu Thr Gly Ile Thr Ala Gly Glu Leu Ser Ala Thr Ser Thr Asp
 2580 2585 2590
 Ala Val Asn Gly Ser Gln Leu Tyr Ala Thr Asn Gln Asn Val Ser Asn
 2595 2600 2605
 Ile Asp Asn Thr Val Ser Asn Leu Ser Asn Asn Val Thr Asn Ile Ala
 2610 2615 2620
 Gly Asn Val Thr Asn Ile Ser Asn Thr Val Asn Asn Ile Thr Asn Gly
 2625 2630 2635 2640
 Gly Gly Gly Ile Lys Tyr Phe His Ala Asn Ser Thr Leu Ala Asp Ser
 2645 2650 2655
 Ser Ala Thr Gly Val Asp Ala Val Ala Ile Gly Gly Asn Ala Gln Ala
 2660 2665 2670
 Thr Ala Ala Asn Ser Val Ala Leu Gly Ser Asn Ser Thr Thr Thr Ala

2675					2680					2685					
Asn	Leu	Ser	Ala	Ala	Gly	Tyr	Asn	Pro	Gly	Thr	Gly	Thr	Leu	Ser	Gly
2690						2695					2700				
Ile	Ala	Ser	Ala	Ala	Asn	Gly	Glu	Val	Ser	Val	Gly	Ala	Ala	Gly	Lys
2705					2710					2715					2720
Glu	Arg	Arg	Val	Thr	Asn	Val	Ala	Ala	Gly	Ser	Ala	Ala	Thr	Asp	Ala
				2725					2730					2735	
Val	Asn	Val	Ser	Gln	Leu	Gln	Ser	Glu	Asp	Ala	Lys	Val	Asn	Thr	Ile
			2740					2745					2750		
Asn	Asn	Asn	Val	Asn	Asn	Leu	Ser	Asn	Asn	Val	Ser	Asn	Ile	Ala	Gly
			2755				2760					2765			
Asn	Val	Thr	Asn	Ile	Ser	Asn	Thr	Val	Asn	Asn	Ile	Thr	Asn	Gly	Gly
	2770					2775					2780				
Gly	Gly	Ile	Lys	Tyr	Phe	His	Ala	Asn	Ser	Thr	Leu	Ala	Asp	Ser	Ser
2785					2790					2795					2800
Ala	Thr	Gly	Thr	Asn	Ser	Leu	Ala	Ala	Gly	Pro	Ala	Ala	Val	Ala	Ser
				2805					2810					2815	
Ala	Thr	Asp	Ala	Val	Ala	Leu	Gly	Asn	Gly	Ala	Lys	Ala	Thr	Asn	Ala
			2820					2825					2830		
Gly	Ala	Val	Ala	Leu	Gly	Ala	Gly	Ser	Thr	Thr	Thr	Thr	Ala	Val	Ala
	2835						2840						2845		
Thr	Ser	Gly	Thr	Thr	Ile	Gly	Gly	Ile	Thr	Tyr	Thr	Phe	Ala	Gly	Val
	2850					2855					2860				
Ala	Pro	Ser	Ser	Thr	Val	Ser	Val	Gly	Ala	Ala	Gly	Ser	Glu	Arg	Thr
2865					2870				2875						2880
Ile	Thr	Asn	Val	Ala	Ala	Gly	Arg	Leu	Ser	Ala	Thr	Ser	Thr	Asp	Ala
				2885					2890					2895	
Val	Asn	Gly	Ser	Glu	Leu	Phe	Ala	Thr	Asn	Gln	Gln	Val	Thr	Arg	Asn
			2900					2905					2910		
Thr	Ala	Asp	Ile	Thr	Asn	Leu	Thr	Asn	Asn	Met	Asn	Ile	Gly	Ser	Val
	2915						2920					2925			
Gly	Leu	Val	Gln	Gln	Asp	Ala	Thr	Thr	Arg	Thr	Ile	Thr	Val	Ala	Lys
	2930					2935					2940				
Ala	Thr	Asp	Gly	Thr	Arg	Val	Asp	Phe	Thr	Gly	Thr	Gly	Gly	Ala	Arg
2945					2950					2955					2960
Gln	Leu	Thr	Gly	Val	Ala	Ala	Gly	Ala	Val	Asn	Ala	Thr	Ser	Val	Asp
				2965					2970					2975	
Ala	Val	Asn	Gly	Ser	Gln	Leu	Tyr	Gly	Val	Ser	Gln	Ser	Val	Ala	Asp
			2980					2985					2990		
Ala	Ile	Gly	Gly	Gly	Ser	Thr	Val	Asn	Thr	Asp	Gly	Ser	Ile	Ser	Ala
	2995						3000					3005			

3010	3015	3020
Ile Ser Asn Leu Asp Asn Arg Val Thr Gln Asn Thr Thr Asp Ile Ser 3025 3030 3035 3040		
Thr Ile Asn Asn Thr Leu Asn Ser Ile Thr Thr Gly Ala Gly Val Lys 3045 3050 3055		
Tyr Val His Val Asn Ser Thr Leu Ala Asp Ser Leu Ala Lys Gly Ala 3060 3065 3070		
Glu Ser Val Ala Ile Gly Gly Asn Ala Gln Ser Gln Ala Ala Asn Ser 3075 3080 3085		
Val Ala Leu Gly Ser Asn Ser Val Ala Asp Arg Ala Asn Thr Val Ser 3090 3095 3100		
Val Gly Ala Ala Gly Ala Glu Arg Gln Ile Thr Asn Val Ala Ala Gly 3105 3110 3115 3120		
Thr Ala Asp Thr Asp Ala Val Asn Val Ala Gln Leu Lys Ala Ser Gly 3125 3130 3135		
Val Ile Asn Thr Asp Gly Thr Thr Asn Ala Ala Val Thr Tyr Asp His 3140 3145 3150		
Asn Ala Asp Gly Ser Ala Asn Tyr Asn Ser Val Thr Met Gly Asn Gly 3155 3160 3165		
Val Ala Gly Gly Thr Thr Ile His Asn Val Ala Ala Gly Ser Ala Ala 3170 3175 3180		
Asp Asp Ala Val Asn Val Ser Gln Met Asn Ala Ala Ile Ser Ser Val 3185 3190 3195 3200		
Ser Asn Ile Ile Gly Ser Ala Gly Asn Pro Leu Phe Thr Ala Asp Gly 3205 3210 3215		
Asn Arg Asp Thr Glu Ala Ala Val Ala Ser Gly Thr His Ala Thr Ala 3220 3225 3230		
Met Gly Ala Asn Ala Lys Ala Ser Ala Ala Asn Ser Val Ala Leu Gly 3235 3240 3245		
Ala Asn Ser Val Ala Asp Arg Glu Asn Thr Val Ser Val Gly Ser Ala 3250 3255 3260		
Gly Asn Glu Arg Gln Val Thr Asn Val Ala Ala Gly Thr Ala Thr Thr 3265 3270 3275 3280		
Asp Ala Val Asn Val Gly Gln Leu Asn Gln Ala Ile Gly Ala Ser Ile 3285 3290 3295		
Gly Asn Leu Pro Ala Gly Met Ser Ala Lys Asp Tyr Thr Asp Gln Gln 3300 3305 3310		
Ile Asn Ala Val Gln Asn Gly Val Asn Gln Val Ala Lys Asn Ala Tyr 3315 3320 3325		
Ala Gly Ile Ala Ala Ala Thr Ala Leu Thr Met Ile Pro Asp Val Asp 3330 3335 3340		
Gln Gly Lys Thr Ile Ala Val Gly Val Gly Gly Gly ser Tyr Lys Gly 3345 3350 3355 3360		

Ser Gln Ala Val Ala Leu Gly Ile Ser Ala Arg Ile Thr Gln Asn Leu
3365 3370 3375

Lys Met Lys Ala Gly Ala Gly Thr Ser Ser Gln Gly Thr Thr Val Gly
3380 3385 3390

Leu Gly Ala Ser Tyr Gln Trp
3395

<210> 18
<211> 577
<212> PRT
<213> Escherichia coli

<400> 18
Met Leu Ile Gln Gln Asn Ser Glu Val Ile Asn Gln Leu Ala Gly Asn
1 5 10 15

Thr Ser Glu Thr Tyr Ile Glu Glu Asn Gly Ala Ser Ile Asn Tyr Val
20 25 30

Arg Thr Asn Asp Thr Gly Leu Thr Phe Thr Asp Ala Ser Ala Ala Gly
35 40 45

Ile Gly Ser Thr Ala Val Gly Tyr Asn Thr Val Ala Lys Gly Asp Asn
50 55 60

Ser Val Ala Met Gly Tyr Asn Ser Phe Ala Glu Gly His Ser Ser Val
65 70 75 80

Ala Ile Gly Gln Gly Ser Tyr Ser Gly Val Glu Thr Ser Ile Ala Leu
85 90 95

Gly Ser Glu Ser Val Ser Ser Arg Val Ile Val Lys Gly Ser Arg Asn
100 105 110

Thr Ser Val Ser Glu Glu Gly Val Val Ile Gly Tyr Asp Thr Thr Asp
115 120 125

Gly Glu Leu Leu Gly Ala Leu Ser Ile Gly Asp Asp Gly Lys Tyr Arg
130 135 140

Gln Ile Ile Asn Val Ala Asp Gly Ser Glu Ala His Asp Ala Val Thr
145 150 155 160

Val Arg Gln Leu Gln Asn Ala Ile Gly Ala Val Ala Thr Thr Pro Thr
165 170 175

Lys Tyr Tyr His Ala Asn Ser Thr Ala Glu Asp Ser Leu Ala Val Gly
180 185 190

Glu Asp Ser Leu Ala Met Gly Ala Lys Thr Ile Val Asn Gly Asn Ala
195 200 205

Gly Ile Gly Ile Gly Leu Asn Thr Leu Val Leu Ala Asp Ala Ile Asn
210 215 220

Gly Ile Ala Ile Gly Ser Asn Ala Arg Ala Asn His Ala Asp Ser Ile
225 230 235 240

Ala Met Gly Asn Gly Ser Gln Thr Thr Arg Gly Ala Gln Thr Asn Tyr
245 250 255

Thr Ala Tyr Asn Met Asp Ala Pro Gln Asn Ser Val Gly Glu Phe Ser
 260 265 270
 Val Gly Ser Glu Asp Gly Gln Arg Gln Ile Thr Asn Val Ala Ala Gly
 275 280 285
 Ser Ala Asp Thr Asp Ala Val Asn Val Gly Gln Leu Lys Val Thr Asp
 290 295 300
 Ala Gln Val Ser Gln Asn Thr Gln Ser Ile Thr Asn Leu Asn Thr Gln
 305 310 315 320
 Val Thr Asn Leu Asp Thr Arg Val Thr Asn Ile Glu Asn Gly Ile Gly
 325 330 335
 Asp Ile Val Thr Thr Gly Ser Thr Lys Tyr Phe Lys Thr Asn Thr Asp
 340 345 350
 Gly Val Asp Ala Asn Ala Gln Gly Lys Asp Ser Val Ala Ile Gly Ser
 355 360 365
 Gly Ser Ile Ala Ala Ala Asp Asn Ser Val Ala Leu Gly Thr Gly Ser
 370 375 380
 Val Ala Asn Glu Glu Asn Thr Ile Ser Val Gly Ser Ser Thr Asn Gln
 385 390 395 400
 Arg Arg Ile Thr Asn Val Ala Ala Gly Val Asn Ala Thr Asp Ala Val
 405 410 415
 Asn Val Ser Gln Leu Lys Ser Ser Glu Ala Gly Gly Val Arg Tyr Asp
 420 425 430
 Thr Lys Ala Asp Gly Ser Ile Asp Tyr Ser Asn Ile Thr Leu Gly Gly
 435 440 445
 Gly Asn Gly Gly Thr Thr Arg Ile Ser Asn Val Ser Ala Gly Val Asn
 450 455 460
 Asn Asn Asp Ala Val Asn Tyr Ala Gln Leu Lys Gln Ser Val Gln Glu
 465 470 475 480
 Thr Lys Gln Tyr Thr Asp Gln Arg Met Val Glu Met Asp Asn Lys Leu
 485 490 495
 Ser Lys Thr Glu Ser Lys Leu Ser Gly Gly Ile Ala Ser Ala Met Ala
 500 505 510
 Met Thr Gly Leu Pro Gln Ala Tyr Thr Pro Gly Ala Ser Met Ala Ser
 515 520 525
 Ile Gly Gly Gly Thr Tyr Asn Gly Glu Ser Ala Val Ala Leu Gly Val
 530 535 540
 Ser Met Val Ser Ala Asn Gly Arg Trp Val Tyr Lys Leu Gln Gly Ser
 545 550 555 560
 Thr Asn Ser Gln Gly Glu Tyr Ser Ala Ala Leu Gly Ala Gly Ile Gln
 565 570 575
 Trp

<210> 19
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> polyglycine linker with BamHI restriction site

<400> 19
 Gly Ser Gly Gly Gly Gly
 1 5

<210> 20
 <211> 1151
 <212> DNA
 <213> Haemophilus aegyptius

<400> 20
 gtaccgcacg agctggcaaa aaaggcacgg cagtctcttt tgtcgaagcc catgattaca 60
 agttgctagg taaaatcaaa cggtatactg aggaaatttt aaaggcacgc atttttagcag 120
 gtttagaacc tcgcactaag ccaccaaaaag atggcggaagt gaaatctgtc agcaaaaaaac 180
 aaaaggcgcg cattaaagaa aaacgtgaag ataagaaaaa aacagaggca aagaaaaaag 240
 taaaattgcg tcataaggat acaaaaaata tcggcaaacg acgcaagcca agtaatagta 300
 atattttaatt aggtatgatg taaattctgc ttgaggcaaa ttttacatag gaaatttttc 360
 tatattgctt taacgttttt ttatagtaga agtatatact cagttatggg tatggttaca 420
 tagtatagtt ttacttttgtt ctagttcact ttaataacct taaataattg aggatttctt 480
 atgaaaagaa attttattaaa acaatctgta atcgctgtgt tgatagggtg cactactgtt 540
 tctaattatg ctttagcaca agcacaagca caagcacaag tcaaaaaaga tgaacttagt 600
 gagttaaaga aacaagtaaa ggaaatggat gctgctatcg atgggtattct tgatgataat 660
 attgcttatg aagctgaagt tgatgcaaaa cttgatcagc attctgctgc tcttggtaga 720
 catacaaata gactcaataa tcttaaaacg attgcagaga aagcaaaagg tgattcaagt 780
 gaagcacttg ataaaattga agctcttgaa gaacaaaatg atgagttttt agcggatatt 840
 acagcttttag aagagggagt tgatgggtta gatgatgata tcgcagggtat tcaagataat 900
 atttctgata tagaagatga tattaatcaa aattctgcag acatcgcaac taacacagcg 960
 gcaatcgcaa ctacactca acgtcttgat aatttagata acagagtaaa taaccttaat 1020
 aaagatctta aacgtgggtc tgctgctcaa gctgcattaa atgggtttatt ccaaccgtat 1080
 aacgtaggta aattaaatct tactgctgct gtaggtgggt ataaatctca aactgcagtt 1140
 gctgtaggta c 1151

<210> 21
 <211> 1359
 <212> DNA
 <213> Haemophilus somnus

<400> 21
 atgaaaaaag tacaattttt taaatattca tcattggcat tagcattggg tttaggggta 60
 agtgcttctg ctttggcagc cccaacaagt acaagtacga ctactggacc agaggcgcct 120
 cctacaggcc ctgctcctac ggcgaaagac cctctagcag aaacagcggt agcctatgat 180
 ttggagaacg aagttgcgta tcttcgtatg aaggcgggtg agtggatgca attggggcct 240
 gatcctgaaa aagaagtcac caaaggctgg aatgaggtaa aatctctccc tcgtatcgat 300
 ggaaatggaa aggataaaca gacaaaagat caaatagcaa tgttgataag aacggttgat 360
 aatacaaaag agcttggtcg gatcgttagt acaaacattg aagatattaa gaaccttaaa 420
 aaagagcttt acggttttgt agaagatgtg aacgagagtg aagcacgcaa tatctcaaga 480
 atagatgaga atgagaaaga tattaagaac cttaaaaaag agctttacga tttttagtaa 540
 gatgtgaacg agagtgaagc acgcaatatc tcaagaatag atgaaaatga gaaggacatt 600
 aatactctta aagagctaag ggatgaggat ttaaattcag tcttaaccca aattgaagat 660
 gtaaaactca catttcaaga tgtcaatgat aacgttaatt tggcatttga agagattaat 720
 ggaaatgccc aaaagtttga cactgctatt gaaggactta cttcagggtt gagcgattta 780
 caagctaaag tcgatgcaaa taaacaagaa actgaagacg atattgcgga caatgccaaag 840
 gctattcata gcaacacaaa aggtattgct aaaaatacca aggatattcg tgacttggac 900
 accaaaacca agcaaatgtt ggaaaatgac aaaaacttga tgaccgggtt agaattctta 960
 gcaacagaaa caagcaaagg ctttgaaaga tttgatgtca aaacacacaa attagatcaa 1020
 gccgtcgcaa atgtcgtcgg tcgagtagac ataactgagc aagctattcg ccaaaacact 1080
 gcaggcttag tcaatgtgaa taaacgtgtc gatacactcg acaaaaacac caaagccggt 1140

atcgcttctg	cagtcgcttt	aggtatgttg	ccacaatcca	ctgctccggg	taaatcatta	1200
gtgagcttag	gtgtcgggtca	tcaccgtggg	caaagtgtca	ctgctattgg	agtatcttct	1260
atgagcagta	acggtaaatg	ggttgttaaa	ggcgggtatga	gctatgatac	acagcgtcat	1320
gctacttttcg	gcggttctgt	cggttttttc	tttaactaa			1359

<210> 22
 <211> 1017
 <212> DNA
 <213> Escherichia coli

<400>	22					
atgaaaactg	taaacgtagc	tttactggca	ctcataat	cagcaacatc	cagccctggt	60
gttttagctg	gtgataccat	tgaagcggcg	gcaacagagc	tttcagccat	taactctggc	120
atgtcgcaat	cggagattga	gcagaagatt	acccgctttt	tagaacgcac	agacaacagc	180
cccgtcgctg	atacctat	gactgaacat	cactacatcc	cttctgaaac	acctgatacc	240
actcagactc	ccactgtcca	gacagatcct	gacgcaggac	aaaaaaccgt	tgccgctaca	300
ggtgatgtac	agacaactgc	ccgttatcag	agcatgatca	acgcccgcga	gtctgcggta	360
actgacgccc	agcaaacgca	aattacagag	caacaggcgc	agatcgtagc	cacacaaaaa	420
acgctcgccg	cgactggaga	tacgcaaaat	accgcgcatt	atcaggaaat	gattaatgcc	480
agactggcgg	ctcaaaatga	ggctaatacag	cgcaccgcca	ctgaacaagg	gcagaaaatg	540
aatgctgctga	caaccgatgt	ggcagtacaa	cagcaaaatg	aaaggactca	atacgataaa	600
caaatgcaaa	gtctggcgca	ggagtctgcc	caggcacatg	aacaaattga	cagcctgtca	660
caagacgtaa	cccaaacgca	ccaacagtta	accaacaccc	aaaaacgggt	tgagataaac	720
agccagcaaa	ttaacacgct	caataacat	ttcagttcgc	taaaaaacga	agttgatgac	780
aatcgtaaaag	aagccaatgc	gggaactgca	tctgccatcg	ctatcgcttc	acaaccacag	840
gttaaaaccg	gtgacgtgat	gatgggtgtca	gcgggagcgg	gaaccttcaa	cgggtgaatct	900
gcgggtgtctg	tcggaacatc	atttaaatgcc	ggaacgcata	cgggtacttaa	agccggtatt	960
tctgcggata	cacaatctga	tttcggcgca	ggtgtcggcg	tgggatattc	gttctaa	1017

<210> 23
 <211> 4860
 <212> DNA
 <213> Escherichia coli

<400>	23					
atcgccaaac	agcgtcggcg	tctggggcgca	gtaagagact	tgctgacggt	agattttctgg	60
cttttagtgtg	ctgacatcct	caccttcaaa	cagtaacggt	ccgctgggtg	ggctgatcaa	120
tgaagcaact	atTTTTtagca	gcgtactttt	gccacaacca	gaaggaccgg	taattaactt	180
aaattcgcca	gcacgcagcg	aaaaattgat	gttattaaga	atcttcgcat	caccgcgccc	240
atatacctacg	ttttgtagct	gaagcaaagg	actatTTTcc	tgcatcgctg	ttcccttttt	300
ctgatttttta	ctaaaaacag	tttatccttc	gcaggaataa	gggggaactc	tctttcagta	360
atcaggtata	atTTgtttta	tcaagcagca	atTTtgctga	ttatggacgg	tacaacagga	420
ggTTTTtccg	atgcttatct	ttatcccgat	tctcatTTTT	gtcgcgctgg	tcattgtcgg	480
cgcgggcgctc	aaaatcgtgc	cgcagggcta	tcaatggacg	gtagaacggt	ttgggtcgcta	540
taccaaAACG	ttacagccgg	ggctcagttc	ggtgggtgccg	tttatggatc	gcattgggtcg	600
caagatcaat	atgatggagc	aagtgtctga	tatcccttcc	caggaagtta	tctcgaaaga	660
taacgccaaac	gttaccatcg	acgcagttctg	TTTTattcag	gtgattgacg	cgccacgcgc	720
ggcttatgaa	gtcagcaatc	tggagctggc	gatcatcaac	ctgaccatga	ctaacatccg	780
taccgtgttg	ggttcaatgg	aacttgacga	aatgtctctc	cagcgcgcga	gcatcaactc	840
acgcctgctg	cgtattgtcg	atgaggccac	caaccgcgtg	gggattaaag	tcaccgcgtat	900
tgaaattcgc	gacgtgcgcc	caccggcgaga	gcttatctct	tcaatgaacg	cgcagatgaa	960
agcggaaacgt	accaaacgcg	cttacattct	tgaagcggaa	gggatccgtc	aggcggaaat	1020
cctcaaagcc	gaaggtgaaa	aacagtcgca	aatcctgaaa	gcggaaggcg	aacgtcagtc	1080
ggcgttttta	caggctgaag	cgcgtgaacg	ttccgctgaa	gcagaagccc	gcgccaccaa	1140
aatgggtgtct	gaagccatcg	cctccgggtga	tattcaggcg	gtgaactact	tcgtagcgca	1200
gaaatacacc	gaagcgttac	agcagatcgg	ttcctccagt	aacagcaaag	tagtgatgat	1260
gccattagag	gccagcagcc	tgatggggtc	gattgccggg	attgccgagc	tggtgaaaga	1320
cagcgccaac	aagcggactc	agccatgatg	gagttaatag	tcgttcatcc	acataTTTTc	1380
tggctcagtc	tcggcggttt	gctgctggca	gccgagatgc	tgggcggaaa	tggttatttg	1440
ttgtggagtg	gcgtggcagc	agtgattact	ggcctgggtg	tctggctgggt	gccgctgggt	1500
tgggagtggtg	aaggggtgat	gtttgccgtc	ctgacgctgc	tcgccgcctg	gctgtgggtg	1560
aaatgggtgtg	cgcggcggtg	gcgcgaacaa	aagcacagcg	acagtcattt	aaaccagcgc	1620
gggcagcagc	tgattggccg	acgtttttgtg	ctggaatctc	cgctgggtcaa	cgggcgcgggt	1680
catatgcgcg	tcgggtgacag	ttcatggcct	gtcagcgcca	gcgaggatct	cggcgcaggt	1740

acgcatgttg	aagtcattgc	gatagaaggg	ataacgctga	tcattccgtgc	ggatcatcgcc	1800
tgatgcgacg	ctgacgcgtc	ttatcatgcc	cggaagtctg	cgcccgaatc	gtaggccgga	1860
taaggcgttt	acgccgcac	cggcagtcgt	gcaccgacgc	ctgatgacgac	gcgggagcgt	1920
catatcacgc	caaaaccgta	ggccgcctcc	gccatgttaa	atgttaaactg	gcattggcaa	1980
tttactcttc	ccggccttta	ctcatacttt	tttgggtcttc	atccggatag	tgttttttta	2040
gatattccag	gacgttttta	ttgaccttgt	gttgcggtata	cacccaccct	ttccagtaat	2100
caggctgggc	caggtaaaact	tctggcgga	tggtgaaatc	agaaagcgtt	aaccattcgg	2160
ctaacagatc	ggggtttcgt	ttctgtatca	actgcaacag	cataatcagc	gacatggcag	2220
aggcaggagc	cgtactatcg	ccgcttaaat	acttccacac	tgtcgaccgg	ttcgaacgaa	2280
aaaggatcgg	tagcaatgcc	cgggccagat	tcattttcatt	aaaaatcttc	tcaaattcat	2340
tcattttaaat	tttcctgcct	ggcgtaaacc	tcttaaaaaat	tgagatttat	caaagaaacg	2400
catttttagca	cacatcagga	accgcttcac	gttttagtcca	gaaacagaat	ttattttcgt	2460
tatcaaaaca	agtcttttact	ctttttttaca	ttgaaagagc	acgaaatgat	ttcctttttt	2520
atttatataa	gaaaccattt	ttgtttctta	ttgatgggtg	ttacgcttac	aacagacaaa	2580
aatgcgcttt	acatcacaca	aatggcgggc	tagatttcga	ttaaattgca	acgcagttta	2640
tttcttaaaa	caatattatt	tggtttcttat	agaaacatta	atacgactta	ttttgaacaa	2700
gagaaaatga	atgaaaactg	taaacgtagc	tttactggca	ctcataattt	cagcaacatc	2760
cagccctgtt	gttttagctg	gtgataccat	tgaagcggcg	gcaacagagc	tttcagccat	2820
taactctggc	atgtcgcaat	cggagattga	gcagaagatt	acccgctttt	tagaacgcac	2880
agacaacagc	cccgtctgct	atacctattt	gactgaacat	cactacatcc	cttctgaaac	2940
acctgatacc	actcagactc	ccactgtcca	gacagatcct	gacgcaggac	aaaaaaccgt	3000
tgccgctaca	ggtgatgtac	agacaactgc	ccgttatcag	agcatgatca	acgcccgcga	3060
gtctgcggtg	actgacgccc	agcaaacgca	aattacagag	caacaggcgc	agatcgtagc	3120
cacacaaaaa	acgctcgccg	cgaactggaga	tacgcaaaat	accgcgcatt	atcaggaaat	3180
gattaatgcc	agactggcgg	ctcaaaaatga	ggctaatacag	cgcaccgcca	ctgaacaagg	3240
gcagaaaatg	aatgcgctga	caaccgatgt	ggcagtagaa	cagcaaaaatg	aaaggactca	3300
atacgataaa	caaatgcaaa	gtctggcgca	ggagtctgcc	caggcacatg	aacaaattga	3360
cagcctgtca	caagacgtaa	cccaaacgca	ccaacagtta	accaacaccc	aaaaacgggt	3420
tgcagataac	agccagcaaa	ttaacacgct	caataaccat	ttcagttcgc	taaaaaacga	3480
agttgatgac	aatcgtaaag	aagccaatgc	gggaactgca	tctgccatcg	ctatcgccctc	3540
acaaccacag	gttaaaaccg	gtgacgtgat	gatgggtgca	gcgggagcgg	gaaccttcaa	3600
cgggtgaatct	gcgggtgtctg	tcggaacatc	atttaatgcc	ggaacgcata	cggtagcttaa	3660
agccggtatt	tctgcggtata	cacaatctga	tttcggcgca	gggtgctggcg	tgggatattc	3720
gttctaatat	ttcaatcctc	aatataaata	agagcaagga	agcttgcccg	gttcacctct	3780
tcattaattt	gtacattatt	taagggttaac	aatgatgaat	agctccatta	aatcgttttc	3840
cctgctggcg	gttatattac	tggtctggctg	tagttcaccc	acttcccgcga	tcgcagattg	3900
ccaggcgagc	ggcgtcagtc	atgacacctg	ttacctcgca	gaacagcagc	gtcaggcggc	3960
tatttttaagt	gcatccgagg	cacaggcatt	taaaaatgca	gaagccgcac	aacacgcccc	4020
ggcggcaaaag	aaagccattt	ataaaggatt	tggtcatgacc	tttagaatga	gcagtaaaaa	4080
ctttgcttat	ctcaatgatt	cattatgtgc	aattgatgaa	gacaataaaag	atgccactgt	4140
ttatcagtca	ggtctatata	acgtcattgt	ttatcatcac	acaggaaaag	tcgccttaat	4200
gaaagaaggc	cagttttgtgg	gttatttttaa	atgaaggagc	aaaggaaaat	acccctgacg	4260
catattatga	ttatcggtgc	gtttatttttt	gccttcttgc	aagtagtatt	attagcctcc	4320
ctggttcacg	ctgtgaatgt	taacaacgaa	atccagggaag	gcttattttca	gtcggggcgc	4380
attatggtag	aaagtttgca	gcataattctt	tcggtgcaaa	cggggattca	ctgatttttca	4440
ccccgcccga	tgatgacagc	agccggagag	atttttcgata	atcgggcagt	cggcgctgtc	4500
atcacccggg	caggcattcg	ccagcgccag	tagctgggtg	cgcatagatt	gcagttcttc	4560
gatatgccgt	tcaatctccg	ccaccttctc	cagcgtgcga	cgtttgacgt	cggcactgtg	4620
acgctgcggg	tcgttaaaca	gattcaccag	ctcgccgctc	tcttccaggt	taaagcccac	4680
ctggcgcgcc	tggcgcagta	aggtcaattc	gttgagatgc	tgctgcgtgt	aggttcgata	4740
accatttttcg	ctgcgcatcg	gcggcgctcac	cagccccttc	tcttcataga	agcgaatggc	4800
tttgctgggc	aggccggtaa	tttttgctac	atcgctaattg	ttcatcgttc	gcgcaacgcc	4860

<210> 24
 <211> 1017
 <212> DNA
 <213> Escherichia coli

<400>	24					
atgaaaactg	taaacgtagc	tttactggca	ctcataattt	cagcaacatc	cagccctttt	60
gttttagctg	gtgataccat	tgaagcggcg	gcaacagagc	tttcagccat	taactcgggc	120
atgtcgcaat	cggagattga	gcagaagatt	acccgctttt	tagaacgcac	cgacaacagc	180
cccgtgcat	atacctattt	gactgaacat	cactacatcc	cttctgaaac	acctgatacc	240
actcagactc	cccctgtcca	gacagatcct	gacgcaggac	aaaaaaccgt	tgccgctaca	300

ggtgatgtac	agacaaccgc	ccgttatcag	agcatgatca	acgccccgaca	gtctacggta	360
actgatgcc	agcaaacgca	aattacagag	caacaggcgc	agatcgtagc	cacacaaaaa	420
acgctcgccg	cgactggaga	tacgcaaaat	accgcgcatt	atcaggagat	gattaatgcc	480
aggctggcgg	ctcaaaatga	ggctaatacag	cgcactacca	cggaacaagg	gcagaaaaatg	540
aatgcactga	caaccgatgt	ggcagcacaa	cagcaaaaag	aaagggtctca	atacgataaa	600
caaatagcaa	gtctggcgca	gaagtctgtc	caggcacatg	agcaaattga	aagtctgaga	660
caagattccg	cacaaacgca	gcaacagtta	accaacaccc	aaaaacgggt	tgcagataac	720
agccagcaaa	ttaacacgct	caataacat	ttcagttcgc	taaaaaacga	agttgaggac	780
aatcgtaaag	aagccaatgc	gggaactgca	tctgccatcg	ctatcgctc	acaaccacag	840
gtgaaaaccg	gtgacttgat	gatggtctca	gcgggagcgg	gaaccttta	cggtgaatct	900
gcggtgtctg	tcggaacatc	ttttaatgcc	ggaacgcata	cggtacttaa	agcaggtatt	960
tctgcggata	cacaatctga	tttcgggtgcg	ggtgtcggcg	tgggatattc	gttctaa	1017

<210> 25
 <211> 2154
 <212> DNA
 <213> Escherichia coli

<400> 25						
atgaaaactg	taaagctgtc	tttactggct	gtcgttgttg	ctaccgcggt	aagtccatct	60
gcgtttgcgg	gtgatactgt	tgaggcggca	acgacagaat	taacggtaat	ccagccagga	120
atgtcgcaat	cggaattga	tcagaaaatt	ggtcgatttt	tagaaaggac	agggaatagt	180
gtagccgcac	aaaattatct	gattgcgcac	gattaccaga	caacgacgcc	tcaggaaaat	240
acagctgctt	ctcccgtaca	gcccaccaat	acgctgaacc	cgataaccaa	tcaagcgcag	300
accgaccgcg	acaacgggca	ggataccgcc	attcaggacg	cgcagcacgc	cgccaactgg	360
gcttcactga	aagctgatga	cgcgcagcac	gccatcacgg	tggcgcagac	ggatattgat	420
gccaatagag	ccgccatcac	cgatacccg	aatgatgtct	ccgcagtgc	gtcagacgtc	480
accaacataa	aaggcgatgt	cgcacatgcc	cagtcaacgg	ctgaccatgc	caacgctaac	540
gccaacaccg	ctctgattaa	cggcgtcaaa	ctttccgggtg	ctgtgacaga	aaacaaaaac	600
aacatcgaac	agaaccgcag	cgatattgct	gaccagcaga	aactgttggc	atcaaacgag	660
caaaaacaga	tcgtccgcga	caacgggcag	gataccgcca	ttcaggacgc	acaacatgcc	720
gccaaactgg	cttacttgaa	agctgatgac	gcgcaacacg	ccatcacggg	ggcgcagacg	780
gatattgatg	ccaataaagc	cgccatcacc	gacatccgta	atgatgtctc	cgcagtgcag	840
tcagacgtca	ccaacataaa	aggcgatgtc	gcacatgccc	agtcaacggc	tgaccatgcc	900
aacgctaacg	ccaacaccgc	tctgatgaac	ggcgtcaaac	tctcctctgc	tgtgacagaa	960
aacaaaaata	atatcgaaca	gaaccgcagc	gatattgctg	accagcagaa	actgttggca	1020
tcaaacgagc	aaaaacagat	cgtccgcgac	aacgggcagg	ataccgccat	tcaggacgca	1080
caacatgccg	ccaactgggc	ttcaatgaaa	gctgatgacg	cgcagcacgc	catcacgggtg	1140
gcgcagacgg	atattgatgc	caataaagcc	gccatcgccg	acaccgta	tgatgtctcc	1200
gcagtgcagt	cagacgtcac	caacataaaa	ggcgatgtcg	cacatgccc	gtcaacgggt	1260
gaccatgcca	acgctaacgc	caacaccgct	ctgattaacg	gcgtcaaa	ttccgggtgct	1320
gtgacagaaa	acaaaaataa	tatcgaacag	aaccgcagcg	atattgctga	ccaacagcaa	1380
caactcgacg	aaaccgggaa	aatcggtgcc	gccaccgggg	atgtgcagac	tgccgcccga	1440
tatcagagca	tgattgacgc	cagacagaca	gccgctgcca	atgcgcaaca	ggcacaagct	1500
gacaccagc	agcaacaaat	ggacgatcag	cagaaacaaa	tcgacgcgac	gcaaaaaacg	1560
gtttccgcac	ttggcgatgc	ccagaccaac	gcacattatc	aagagatggg	taacgccgga	1620
ctgagagcac	aaaatgatgc	gaatgcgcgt	actgcagcag	aacaaaaaca	aaaaatagat	1680
actctggcga	ctaaccaggc	aacgcaacag	catatcaata	gtgtgcagta	cggggaacaa	1740
attcagcgtc	tggcgcaaga	ctcaacacaa	acgcatgaac	aaattgacag	cctgacacaa	1800
gacgtaaccc	aaacgcatca	gcagttaagc	aacacgcaaa	aacgagtagc	ggataatagc	1860
cagcagatta	ctacgctcaa	taaccatttc	agttcgctga	aaaacgaagt	tgaggacaac	1920
cgtaaagaag	ccaatgcggg	aactgcatca	gccatcgcta	tcgcctcaca	accacaggtg	1980
aaagccgggtg	actttatgat	gatgtcagcg	ggagcgggaa	ccttcaacgg	tgaatctgcg	2040
gtgtctgtcg	gaacatcttt	taatgccgga	acgcataaccg	tgattaaagc	cggtgtctct	2100
gcggatacgc	aatctgattt	cggcgcgggt	gtcggcgtgg	gatattcttt	ctaa	2154

<210> 26
 <211> 5337
 <212> DNA
 <213> Escherichia coli

<400> 26						
atgaacaaaa	tatttaaagt	tatctggaat	ccggcaacag	gcagttacac	cgttgccagc	60
gaaacggcga	agagccgtgg	taaaaaaagc	gggcgcagta	agctgttaat	ttctgcactg	120

gttgcggggtg	ggttggtgtc	gtcgttttggg	gcaagtgcag	ataattacac	tgggcagcca	180
actgattatg	gcgatggctc	agcaggtgac	ggctggggtt	ctatcggtaa	aggggcaaaa	240
gcaaatacct	ttatgaacac	tagtggcgcg	agtacagctt	taggatatga	cgcgatagcc	300
gaaggtgagt	acagttctgc	catcgggtca	aaaacccttg	caactgggtg	agcatccatg	360
gcgttcgggg	ttagtgc aaa	agcaatgggt	gacagaagtg	tcgcgctagg	tgcattcgtca	420
gtagcaaatg	gcgatcggtc	gatggctttt	ggtcggttac	caaagacgaa	tggttttaca	480
tctcttgcta	ttggggactc	ctcccttgcc	gatggtgaaa	aaactattgc	gttaggaaat	540
acggcta aa	cttacgaaat	tatgagcatc	gccctcgggt	ataatgccaa	tgcgtcaaaa	600
gagtatgcaa	tggcgctggg	agcaagtagc	aaagctggcg	gtgctgatag	cctcgcattc	660
ggcagaaaat	ctacagctaa	tagcactggc	tcactggcaa	taggtgctga	cagtagcagt	720
tcgaacgata	acgccatcgc	gatagggaac	aaaacgcaag	ccctgggagt	gaattc gatg	780
gccctgggta	atgcaagtca	ggcatctggc	gaatccagta	ttgcattagg	taacaccagt	840
gaagccagcg	aacaaaatgc	gattgcgctg	gggcaaggta	gcattgcaag	caaagtgaac	900
tcaatcgctg	tgggaagtaa	cagtttgtcc	tcgggagaga	atgccatcgc	attgggagag	960
ggtagtgccg	ctgggtggcag	caacagcctt	gctttcggta	gccagtcagg	ggcaaacggc	1020
aatgattctg	tcgccatcgg	tgtaggggct	gcagcagcga	ccgacaattc	tgtcgcctatc	1080
ggcgaggat	cgaccacaga	tgcaagcaat	acggtttcag	ttggcaacag	cgcaacaaaa	1140
cgcaaaattg	ttaatatggc	tgctggtgcc	ataagcaaca	ccagtaccga	tgccatcaac	1200
ggctcacagc	tttatacgat	cagtgattca	gtcgccaagc	gactcggagg	aggcgctact	1260
gtaggcagcg	atggcaccgt	aaccgcagta	agctacgcgt	tgagaagcgg	aacctataat	1320
aacgtgggtg	atgctctgtc	aggaatcgac	aataataccc	tacaatggaa	taaaaccgcg	1380
ggggcgttca	gcgccaatca	cggtgcaaat	gccaccaaca	aaatcactaa	tgttgctaaa	1440
ggtacggttt	ctgcaaccag	caccgatgta	gtaaacggct	ctcaattgta	cgacctgcag	1500
caggatgctc	tgttgtggaa	cggcacagca	ttcagtgccg	cacacggcac	cgaagccacc	1560
agcaaaatca	ctaacgtcac	cgctggcaac	ctgactgccg	gcagcactga	cgccgttaac	1620
ggctctcagc	tcaaaaccac	caacgacaac	gtgacgacca	acaccacca	catcgccact	1680
aacaccacca	atatcaccaa	cctgactgac	gctgttaacg	gtctcgggtg	cgactccctg	1740
ctgtggaaca	aagcagctgg	cgcattcagc	gccgcgcacg	gcaccgaagc	caccagcaaa	1800
atcaccaacg	tcaccgctgg	caacctgact	gccggtagca	ctgacgccgt	taacggctcc	1860
cagctcaaaa	ccaccaacga	caacgtgacg	accaacacca	ccaacatcgc	cactaacacc	1920
accaatatca	ccaacctgac	tgacgtggtt	aacggtctcg	gtgacgactc	cctgctgtgg	1980
aacaaaacag	ctggcgctatt	cagcgccgcg	cacggcactg	acgccaccag	caagatcacc	2040
aacgtcaccg	ctggcaacct	gactgcccgc	agcactgacg	ccgttaacgg	ctcccagctc	2100
aaaaccacca	acgacaacgt	gacgaccaac	accaccaaca	tcgccactaa	caccaccaat	2160
atcaccaacc	tgactgacgc	tggttaacgg	ctcgggtgacg	actccctgct	gtggaacaaa	2220
acagctggcg	cattcagcgc	cgcgcacggc	actgacgcca	ccagcaagat	caccaatgtc	2280
aaagccgggtg	acctgacagc	tggcagcact	gacgccgtta	acggctctca	gctcaaaacc	2340
accaacgata	acgtgtcgac	caacaccacc	aacatcacca	acctgactga	cgctgttaac	2400
ggtctcggtg	acgactccct	gctgtggaac	aaaacagctg	gcgcattcag	cgccgctcac	2460
ggcactgacg	ccaccagcaa	gatcaccaat	gtcaaagccg	gtgacctgac	agctggcagc	2520
actgacgccg	ttaacggctc	ccagctcaaa	accaccaacg	ataacgtgtc	gaccaacacc	2580
accaacatca	ctaacctgac	ggattccggt	ggcgacctta	aggacgattc	tctgctgtgg	2640
aacaaagcgg	ctggcgctatt	cagcgccgcg	cacggtagcg	aagctaccag	caagatcacc	2700
aacttactgg	ctggcaagat	atcttctaac	agcactgatg	ccattaatgg	ctcacaactt	2760
tatggcgtag	cggattcatt	tacgtcatat	cttggtgggtg	gtgctgatat	cagcgatagc	2820
ggtgtattaa	gtggggccaac	ctacactatt	ggtgggtactg	actacactaa	cgtcgggtgat	2880
gctctggcag	ccattaacac	atcatttagc	acatcactcg	gcgacgccct	actttgggat	2940
gcaaccgcag	gcaaattcag	cgccaaacac	ggcattaata	atgctcccag	tgtaatcact	3000
gatgttgcaa	acggtgcagt	ctcgtccacc	agcagcgacg	ccattaacgg	ttcacaactt	3060
tatggtgtta	gtgactacat	tgccgatgct	ctgggcggga	atgctgtggt	gaacactgac	3120
ggcagtatca	ctacaccaac	ttatgccatc	gctggcgggca	gttacaacaa	cgtcgggtgac	3180
gcgctggaag	cgatcgatac	cacgctggat	gatgctctgc	tgtgggatac	aacagccaat	3240
ggcggtaacg	gtgcatttag	cgccgctcac	gggaaagata	aaactgccag	tgtaatcact	3300
aacgtcgcta	acggtgcagt	ctctgccacc	agcaacgatg	ccattaatgg	ctcacagctc	3360
tatagcacta	ataagtacat	cgctgatgcg	ctgggtgggtg	atgcagaagt	caacgctgac	3420
ggtactatca	ctgcaccgac	ttacaccatt	gcaaataaccg	attacaacaa	cgtcgggtgaa	3480
gccctggatg	cgctcgataa	taacgcgctg	ctgtgggatg	aagacgcagg	tgccataaac	3540
gccagccatg	atggcaatgc	cagcaaaatc	accaacggtt	cggtgggtga	tctctccaca	3600
accagtaccg	atgctgttaa	cggttcccag	ttaaacgcaa	ccaatattct	ggttacgcaa	3660
aatagccaaa	tgattaacca	gcttgctggt	aacactagcg	aaacctacat	cgaggaaaac	3720
ggtgcgggta	ttactatgt	acgtaccaac	gacagcggt	tagcgttcaa	cgatgccagc	3780
gcttcaggta	ttggcgctac	agctgtaggt	tataacgcag	ttgcctctca	tgccagcagt	3840
gtagccatcg	gtcaggacag	catcagcgaa	gttgatacgg	gtatcgctct	gggtagcagt	3900
tccgtttcca	gccgtgtaat	agttaaaggg	actcgtaaca	ccagcgctatc	ggaagaaggt	3960

gttgatgattg	gttatgacac	cacggatggc	gaactgcttg	gcgcggttgc	gattggtgat	4020
gacggtaaat	atcgtcaa	catcaacg	gcggatgg	ctgaagcca	tgatgcggtc	4080
actgttcgcc	agttgcaaaa	cgccattggt	gcagtcgcaa	ccacaccaac	caaatactat	4140
cacgccaact	caacggctga	agactcactg	gcagtcggtg	aagactcgct	ggcaatgggc	4200
gcgaaaacca	tcgttaatgg	taatgcgggt	attggtatcg	gcctgaacac	gctggttctg	4260
gctgatgcga	tcaacgggtat	tgctatcggt	tctaacgcac	gcgcaaatca	tgccgacagc	4320
attgcaatgg	gtaatgggttc	tcagactacc	cgtgggtgcg	agaccaacta	cactgcctac	4380
aacatggatg	caccgcagaa	ctctgtgggt	gagttctctg	tcggcagtga	agacgggtcaa	4440
cgtcagatca	ccaacg	agcagggttcg	gcggataccg	atgcgggttaa	cgtgggtcag	4500
ttgaaagtaa	cggacgcgca	ggtttcccag	aatacccaga	gcattactaa	cctgaacact	4560
caggtcacta	atctggatac	tcgcgtgacc	aatatcgaaa	acggcattgg	cgatatcgta	4620
accaccggta	gcactaagta	cttcaagacc	aacaccgatg	gcgcagatgc	caacgcgcag	4680
ggtaaagaca	gtgttgcgat	tggttctggt	tccattgctg	ccgctgacaa	cagcgtcgca	4740
ctgggcacgg	gttccgtagc	agacgaagaa	aacaccatct	ctgtgggttc	ttctaccaac	4800
cagcgtcgta	tcaccaacgt	tgctgcccgt	gttaatgcc	ccgatgcgg	taacgtttcg	4860
caactgaagt	cttctgaagc	aggcggcggt	cgctacgaca	ccaaagctga	tggtctctatc	4920
gactacagca	acatcactct	cggtggcggc	aatagcggt	cgactcgcat	cagcaacggt	4980
tctgctggcg	tgaacaacaa	cgacgcagtg	aactatgcgc	agttgaagca	aagtgtgcag	5040
gaaacgaagc	aatacaccga	tcagcgcagtg	gttgagatgg	ataacaaact	gtccaaaact	5100
gaaagcaagc	tgagtgggtg	tatcgcttct	gcaatggcaa	tgaccggtct	gccgcaggct	5160
tacacgccgg	gtgccagcat	ggcctctatt	ggtggcggt	cttacaacgg	tgaatcggt	5220
gttgcttttag	gtgtgtcgat	ggtgagcgcc	aatggtcggt	gggtctacaa	attacaaggt	5280
agtaccaata	gccagggtga	atactccgcc	gcactcggtg	ccggtattca	gtggtaa	5337

<210> 27
 <211> 4767
 <212> DNA
 <213> Escherichia coli

<400> 27						
atgaacaaaa	tatttaaagt	tatctggaac	cctgcgacag	ggaattatac	tgttaccagc	60
gaaacggcaa	aaagccgtgg	caagaaatct	gggcgcagta	agctgttaat	ttctgcgctg	120
gttgcggggtg	gaatgttgtc	gtcgttttggg	gcattggcga	atgccgggaa	tgacaacggt	180
cagggtgttg	attacggtag	tggtatcagct	ggcgacggct	gggttgctat	aggcaaagg	240
gcgaaagcaa	atacttttat	gaacaccagt	ggttccagta	ctgctgtggg	ttatgacgct	300
atagctgaag	gccaatatag	ctctgccatc	gggtcaaaaa	cccatgcgat	tggtggtgca	360
tcaatggcct	ttgggggttag	tgcaatatca	gaaggcgata	gaagtatagc	actgggtgcc	420
tcttcgtatt	cattgggccca	atactcaatg	gccctcggcc	gttattcaaa	agcattgggt	480
aaattgtcta	ttgctatggg	ggactcttcc	aaagcgggag	gagcaaacgc	cattgccctg	540
ggaaatgcca	ctaaagctac	tgagattatg	agtattgctc	ttggcgacac	cgccaatgcg	600
tcaaaagcgt	attcaatggc	gctggggagca	agtagcgtcg	catctgaaga	aaacgctatt	660
gcgataggtg	ctgagaccga	agccgctgaa	aatgcaactg	ctattggcaa	taatgcgaag	720
gcaaaaggga	ctaatagcag	ggcaatgggg	ttcggaagcc	ttgccgataa	agtcaatact	780
atcgcattag	gaaatggcag	ccaggctctg	gcagataatg	caatcgccat	aggccagggc	840
aacaaagctg	atggcgtgga	tgccatcgct	ctgggtaatg	gtagccagtc	gagaggctta	900
aacaccattg	ccttaggcac	agccagtaat	gcaactgggtg	ataagagtct	tgcgcttggt	960
agtaatagca	gtgccaacgg	tattaactct	gtcgcgctgg	gcgcagattc	cattgcggat	1020
ttagacaata	ccgtctctgt	cggcaatagt	tcattaaaac	gcaagatcgt	taatgtgaaa	1080
aatggcgcgga	tcaagtctga	cagttacgat	gccattaatg	gttcacagct	ttatgccatt	1140
agcgactcgg	tagcaaaaag	gcttgaggga	ggggtgcag	tagatgttga	tgacggtact	1200
gttacagcac	caacctacaa	tttaaaaaat	ggtagcaaaa	ataacgtagg	ggctgcgctc	1260
gctgtacttg	atgaaaacac	cctgcaatgg	gaccaaacca	aaggcaataa	cagcgtgct	1320
catggtacta	gtagcccaac	tgccagcgta	atcaccgatg	ttgcggatgg	cacgatttca	1380
gcctccagta	aggatgcggt	taacggttcc	caactgaaag	ctaccaatga	cgatgtcgaa	1440
gccaacaccg	ccaatatcgc	tactaatacc	agcaacattg	ccacgaatac	ggcaaatatt	1500
gccaccaata	ccaccaatat	caccaacctg	acggattccg	ttggtgacct	tcaggctgat	1560
gccctgctct	ggaacgaaac	taaaaaggca	ttcagtgcag	ctcacggcca	ggataccacc	1620
agcaaaatca	ccaacgttaa	agatgccgac	ctgacggctg	acagcactga	tgctgttaac	1680
ggctctcagc	tgaaaaccac	caacgatgct	gtggcgacga	ataccaccaa	tatcgccaat	1740
aacacttcca	atattgccac	taacaccacc	aacatctcta	acctgactga	gacgggtgact	1800
aatctttggtg	aggatgcgct	gaaatgggat	aaggacaatg	gtgtattcac	ggcagctcat	1860
ggcaccgaga	ccaccagcaa	aatcaccaac	gttaaagatg	gcgacctgac	kactggcagc	1920
accgatgccg	ttaacggctc	tcagctgaaa	accaccaacg	atgccgtggc	gacgaatacc	1980
accaatatcg	ccactaacac	caccaacatc	tctaattctga	ctgagacggg	gactaatctt	2040

ggtgaggatg	cgctgaaatg	ggataaggac	aatgggtgtct	tactgcagc	tcatggcaac	2100
aataccgcca	gcaaaatcac	caatatcctg	gacggcacag	tactgcaac	cagttccgat	2160
gccattaacg	gtagccagct	ttatgactta	agcagcaata	tcgccaccta	cttcggcggc	2220
aatgcttctg	tgaatactga	cggtgtgttt	accgggtccaa	cctacaaaat	cggtgaaaca	2280
aattattata	acgtcggcga	tgcactggct	gcgattaact	cctcatttag	cacgtctctc	2340
ggcgatgctc	tgctttggga	tgccaccgca	ggtaaattca	gtgccaaaca	cggtactaat	2400
ggtgacgcaa	gcgtgatcac	tgatgtcgca	gatggtgaaa	tttcagactc	cagttctgac	2460
gcagtaaacg	gctcacaact	ccacggcgtg	agcagttatg	ttgttgatgc	gctggggggg	2520
ggtgccgaag	tcaatgcaga	cggcaccatc	actgcgccga	cgtacaccat	tgctaattgct	2580
gattacgata	atgtcgggtga	tgccctgaat	gctatcgata	ccactcttga	cgacgctctg	2640
ctctgggatg	cggacgccgg	tgaaaatggg	gcatttagcg	ccgctcacgg	aaaagataaa	2700
actgccagtg	taatcactaa	cgctcgctaac	ggtgcaatct	ctgctgccag	cagcgacgcg	2760
attaacggct	cacaactcta	taccaccaat	aagtacatcg	ctgatgcgct	gggtgggtgac	2820
gcagaagtca	acgtcgacgg	caccatcacc	gcaccgactt	acaccattgc	gaacgccgag	2880
tacaacaacg	tcggtgacgc	cctggatgcg	cttgatgata	acgccctgct	gtgggatgag	2940
actgccaatg	gcgggtgctgg	agcctacaat	gccagccatg	acggtaaagc	cagcatcatc	3000
actaatgtcg	ctaattggcag	tattagttag	gacagtaccg	atgcagtga	cggttctcag	3060
ttgaatgcga	cgaatatgat	gattgagcag	aacacccaaa	ttatcaatca	gctcgctggg	3120
aacaccgacg	caacctatat	cgaagaaaac	ggcgcggtga	ttactatgt	gcgtactaac	3180
gacgacggct	tagcgttcaa	cgacgccagc	gcacaggggtg	ttggcgctac	agctataggt	3240
tataactctg	tcgccaaagg	cgatagcagc	gtagctattg	gtcagggcag	ctacagcgac	3300
gttgatacgg	gtatcgccct	gggtagcagc	tctgtttcca	gccgagtgat	tgccaaaggc	3360
tcccgtgaca	ccagcataac	ggaaaatggc	gttgttattg	gttacgacac	cacggatggc	3420
gaactgctcg	gtgcattgtc	tatcgggtgat	gacggtaaat	atcgtcaaat	catcaacgta	3480
gccgatgggt	ccgaagccca	tgacgccggt	acggttcgtc	aattgcagaa	tgcgattggg	3540
gcggtcgcaa	ccacgccgac	taaatacttc	cacgctaatt	caacggaaga	agattcactg	3600
gcagtgggaa	ctgactcgct	ggcaatgggt	gcgaaaacca	tcgtgaatgg	cgataaagg	3660
attgggtatcg	gttatgggtgc	ctacgtggac	gcgaatgcac	ttaacggcat	tgccattggg	3720
agcaatgcgc	aagtcattca	tgtcaacagt	attgcatag	gtaatgggtc	tacgaccact	3780
cgtggcgctc	aaaccaatta	taccgcctac	aacatggacg	caccgcagaa	ctctgtcggg	3840
gaattctcag	tcggtagtgc	ggatgggtcaa	cgtcagatca	ctaactgcgc	agcagggttcg	3900
gctgataccg	atgcgggtcaa	cgtgggtcag	ttgaaagtaa	cggatgcgca	ggtttcccag	3960
aatacccaga	gcattactaa	cctggataat	cgggtaacga	atcttgattc	acgcgtcacc	4020
aatatcgaaa	acgggtattgg	cgatatcgct	accaccggta	gcaccaagta	cttcaagacc	4080
aataccgatg	gtgtagatgc	cagcgcgag	ggtaaagata	gcgtcgcgat	tggttcgggc	4140
tccattgctg	ccgctgacaa	cagcgctcgt	ctgggtacag	ggctctgtggc	aaccgaagaa	4200
aatacgaatc	ctgtagggttc	ctctactaac	caacgtcgta	tcaccaacgt	agctgcaggt	4260
aaaaatgcta	ccgatgctgt	taacgtggca	cagttgaagt	cttccgaagc	tggcgggtgta	4320
cgttacgaca	ccaaagctga	tggttctatc	gactatagca	atatcaccct	cggtggcggc	4380
aacggcggtg	cgactcgat	cagcaacgtc	tccgctggcg	tcaacaacaa	cgacgtgggtg	4440
aattacgcgc	agttgaagca	aagcgtgcag	gaaacgaagc	aatacaccga	tcagcgaatg	4500
gttgagatgg	ataacaaact	gtctaaaact	gaaagcaagt	tgagcgggtg	tatcgcttct	4560
gcaatggcaa	tgaccgggtct	gccgcaggct	tacactccag	gtgccagcat	ggcctctatt	4620
ggtggcggtg	cttacaacgg	tgaatcggca	gttgcttttag	gtgtatcgat	ggtgagcgcc	4680
aatggtcggt	gggtctacaa	attacaagg	agtaccaata	gccagggtga	atactccgcc	4740
gcactcgggtg	ccgggtattca	gtgggtaa				4767

<210> 28
 <211> 5232
 <212> DNA
 <213> Escherichia coli

<400> 28						
atgaacaaaa	tttttaaagt	tatctggaat	ccggcaacag	gcagttacac	cggtgccagt	60
gaaacggcaa	aaagccgtgg	caagaaatcc	gggcgcagta	agctgttaat	ttctgccctg	120
gttgctgggg	gaatgttggtc	gtcgttttggg	gtacaggctc	aggcaggaag	ggacaacggg	180
cagggcgtca	attatggcca	gggaacagga	acaggctggg	ttgctatcgg	tgaagatgca	240
aaagcaaata	gttttacaga	caccgggggt	ggctccagca	ccgcagtagg	ttatcactca	300
actgctgacg	gaagggtggc	aacagccctc	ggtgctaaga	cccattcgct	tggcgaagca	360
tcagtggcgt	tagggattaa	cactacctca	gcagggtgagc	gaagcctcgc	tatagggtgca	420
tcggcaacgt	caacgggtgg	atthttcaatc	gcacttggtc	gttatgcgaa	ctcagtaggt	480
gaattttcta	ttgcacaagg	ggatcacgca	gagactgggtg	ctgatgacgc	catcgcatth	540
ggacgtgaaa	gcaaggcctt	aggaattatg	agtatcgccc	tcggagccac	ggctaattgcg	600
tcgaaagaat	atgcaatggc	gctgggtgca	agtagcgccg	catctgcagc	taacgcgatt	660

gcagtaggcc	gcaacagtgc	tgcagctggc	gtagacagcc	tcgcattcgg	cagacaatcc	720
gccgccagcg	ccgcaaacgc	gattgctatg	ggtgcagaga	gcaaagctgc	tgaaaatgcg	780
acggcagttg	gtactaacgc	ggaggcaa	ggacttaata	gtatcgcggt	gggctccggc	840
agtattgcag	atgtcgacaa	cacgattgct	ctgggcaatc	aaagtcaggc	agtagcggct	900
ggcgcaattg	ccatcggtca	agggaataaa	gctgacggcg	caaatgctat	cgcgctgggt	960
aatggtagta	ttacaggtgg	tgtaaatgct	attgctcttg	gacaaggcag	ttatgccggg	1020
ttagaaaatg	gcactgcaat	tggtgctcaa	gccagtgtc	aggggaaaaa	ttcagttgct	1080
ctgggtgctg	gttctgtagc	gactgacgcg	gatactgttt	ctgtgggtaa	cacaacagct	1140
cagcgacaaa	ttgtcaatat	ggcagcaggt	gatatacagc	ctaccagtac	tgatgccatc	1200
aatggatcac	agctttatgc	tatcagtaag	tcagtagcgg	acaatcttgg	tgggggggct	1260
accgtcaatg	cgcaaggcgt	cgttacttcc	ccaaattaca	ggctgaaaag	tggtattttc	1320
ggcactgttg	gcgacgcctt	aacgggcctg	gacaataata	cgttacaatg	ggactccctt	1380
aaaaaggcat	atagtgcggc	acatggtaca	gatactacca	gtaccatcac	caacgttaaa	1440
gacggcgcta	tttctgatac	cagtaaggat	gcggttaacg	gttctcagct	gaaaaccacc	1500
aacgataacg	tagcgaccaa	tactgccaat	atcaccacca	acactaacag	tatcaatacc	1560
ctgacggatt	ccgttggcga	ccttaaagac	gatgccctgc	tgtggaatgg	caccgcgttc	1620
agcgccgcgc	acggcaccga	agccaccagc	aaaatcacca	acgtcaaaga	cggtgacctg	1680
acggctggca	gcaccgacgc	ggttaacggc	tctcagctca	aaaccactaa	cgataatgtg	1740
gcaaccaaca	ccaccaacat	caccaacctg	acggattccg	ttggcgacct	taaagacgat	1800
gccctgctgt	ggaatggcac	cgcgttcagc	gccgcgcacg	gtaccgatgc	caccagcaaa	1860
atcaccaacg	tcaaagacgg	tgacctgacg	gctggtagca	ctgacgcggg	aaacggctct	1920
cagctgaaaa	ccactaacga	tgccgtggca	gccaacacca	ccaatatcgc	cacgaatacc	1980
accaacatca	ccaacctgac	tgacgcagtt	gacagcctcg	gtgacgattc	cctgctgtgg	2040
aacgctacag	cgggggcatt	cagcgccgca	cacgggtactg	atgccaccag	caaaatcacc	2100
aacgtcaccg	ctggcgacct	gacggctggc	agcaccgacg	cggttaacgg	ctctcagctc	2160
aaaaccacta	acgatgccgt	ggcagccaac	accaccaata	tcgccacgaa	caccaccaac	2220
atcaccaacc	tgactgacgc	tgttgacagc	ctcggtgacg	attccctgct	gtggaacgct	2280
actgcggggg	cattcagcgc	cgcgcacggg	actgatgcca	ccagcaaaat	cactaacgtc	2340
aaagacgggtg	acctgacggc	tggcagcact	gacgcggtta	acggctctca	gctcaaaacc	2400
actaacgatg	ccgtggcagc	caacaccacc	aatatcgcca	cgaacaccac	caacatcacc	2460
aacctgactg	acgctgttga	cagtctcggt	gacgattccc	tgctgtggaa	cgctacggcg	2520
ggtgcattca	gtgccaaaca	cggcaccaac	ggtactgaca	gcaaaatcac	caacttactg	2580
gcaggcactg	tatcctctga	tagcactgac	gctattaatg	gctcacaact	ttatggctta	2640
gctgattcat	ttacgtcata	ccttggcggt	ggtgctgata	tcagcgatgc	gggtgtatta	2700
accgggccaa	cctacactat	tggtgggtact	gattacaata	acgtcggtga	tgctctggct	2760
gccattaaca	cgtcatttag	cacatcactc	ggtgacgccc	tactctggga	tgcgaccgcc	2820
aaggcggtg	acgggtgcgtt	tagcgccggt	cgcgggacag	ataacacagc	cagcatcatt	2880
actaatgttg	cagacgggtgc	aatttcctct	accagcagcg	acgctattaa	cggtcacag	2940
ctctatgaca	ccagcaagta	cattgcccga	actctgggtg	gtgacgcaga	agtcaatgct	3000
gacggcacaa	tcaccgcacc	gacttatgcc	atcgctggcg	gcagttacag	caacgtcggg	3060
gacgcgctgg	aagcgatcga	taccacgctg	gatgacgctc	tggtgtggga	tgcaacagcc	3120
aatgatggca	atggtgcatt	tagcgccgct	cacggaaaag	ataaaacagc	cagtgtaatc	3180
actaacgtcg	ctaacgggtgc	aatctctgcc	accagcagcg	atgccattaa	cggttcacaa	3240
ctgtatacca	ccaacaagta	cattgcccga	gccctgggtg	gtgacgcaga	agttaacgct	3300
gatggttcta	ttactgcgcc	gacttacacc	attgcaa	ccgagtacaa	caacgtcggg	3360
gacgccctgg	atgcgctcga	cgataacgct	ctgctgtggg	atgcaacagc	caatgacggc	3420
gcaggtgcct	acaacgccag	ccatgacggc	aaggccagca	tcatcacaaa	tggtgctgat	3480
ggtaacattg	gcgaaggcag	cactgacgcc	atcaacgggt	ctcagctggt	taacaccaat	3540
atgctgatcc	agcagaacag	cgaaatcatc	aatcagcttg	ccggtaacac	cagcgaaacc	3600
tacatcgaag	ataacgggtgc	gggcattaac	tatgtacgta	ccaacgacaa	cggttagcgc	3660
ttcaacgatg	ccagcgcttc	aggattatgg	gctacggctg	tggtttataa	cgctgtcgcc	3720
tcaggcgaaa	gcagcgtagc	cattgggtcaa	ggtagcagca	gcaacgttga	tacgggtatc	3780
gccctgggta	gcagttccgt	ttccagccgt	gtaatagtta	aaggttctcg	tgacaccagc	3840
gtgtcggaag	aagggtgttg	gattgggttat	gacaccacgg	atggcgaaact	acttgggtgcg	3900
ttgtctattg	gtgatgacgg	taaatatcgt	caaatcatca	acgtagccga	tggttccgaa	3960
gcccattgacg	ccgttacggg	tcgccagttg	caaaatgcc	ttggtgcagt	cgctaccacg	4020
ccgaccaa	acttccacgc	caactcaacg	gaagaagatt	cactggcagt	aggatgaagac	4080
tcgctagcaa	tgggcgcgaa	aactatcggt	aatggtaatg	cggttattgg	tatcggttat	4140
ggtgcctacg	tggacgcgaa	tgactttaat	ggcattgcta	tcggtagcaa	cgcgcggtgca	4200
aaccatgcaa	acagcattgc	tatgggtaat	ggctcacaga	cgactcggtg	tgctcaaact	4260
ggctacgccg	cctacaacat	ggacgcaccg	cagaactctg	tgggtgagtt	ctctgtcggc	4320
agtgaagacg	gtcaacgtca	gatcaccaac	gtcgcggtg	gttcggctga	taccgatgcg	4380
gttaacgtgg	gtcagttgaa	agtaacggac	gcgcagggtt	cccagaatac	ccagagcatt	4440
actaacctga	acaatcaggt	cactaatctg	gatactcgcg	ttactaatat	cgaaaacggg	4500

attggcgaca	ttgtaaccac	cggtagcacc	aagtacttca	agaccaacac	cgatggcgta	4560
gatgccaacg	cgcagggtaa	agatagtgtt	gcgattgggt	ctggttccat	tgctgccgct	4620
gacaacacg	tcgcgctggg	tacaggctcc	gtggccaacg	aagaaaatac	catctctgtg	4680
ggttcttcta	ccaaccagcg	tcgtatcacc	aacgttgctg	caggtgttaa	tgccaccgat	4740
gcggttaacg	tttcgcagct	gaagtcttct	gaggcaggcg	gcgttcgta	cgacaccaaa	4800
gctgatggct	ctgtagacta	cagcaacatc	actctcgggt	gtggtaatgg	cggtacgact	4860
cgcatacagca	acgtctccgc	tggcgtgaac	aacaacgacg	cagtgaacta	tgcgagctg	4920
aagcaaagcg	tgcaggaaac	gaagcaatat	accgatcagc	ggatggttga	gatggataac	4980
aaactgtcca	aaaccgaaag	caagttgagc	ggtggtatcg	cttctgcaat	ggcaatgacc	5040
ggtctgccgc	aggcttacac	tccaggtgcc	agcatggcct	ctattgggtg	cggtacttac	5100
aacggtgaat	cggctgttgc	tttaggtgtg	tcgatgggtg	gcgccaatgg	tcgttgggtc	5160
tacaaattac	aaggtagtac	caatagccag	ggtgaatact	ccgccgcact	cggtgccggt	5220
attcagtggt	aa					5232

<210> 29
 <211> 10200
 <212> DNA
 <213> Burkholderia fungorum

<220>
 <221> n
 <222> 2359
 <223> n is any nucleotide

<400>	29					
atgaacaaga	catatcgctc	cgtctggaac	gagtcgacag	gcacttgggt	cgctgcgtcg	60
gaacatgcaa	gtgcacgcgg	gaaaaaatct	tctgcgaaaa	cctcttccac	taaggcagtc	120
gtcggggcgt	tgggtctggc	agccgggcta	tatggtgccg	acgcgtttgc	gctgggtgga	180
gggctaacc	tttgtccgac	caccgaagga	tccgccgggt	acactgccgg	tagcgcttct	240
agcgcaaacg	gggcttactg	cgggtccgac	tatcaatggg	gtttgttcag	caacaccaat	300
gccgacggca	gtaaaagcgg	ccagccgatt	ggtgccgcga	ttgagggaat	gaatgacggc	360
tcattgctgt	tgtacgggtc	caacaacatt	gtgatgaaga	acctgggtcag	catgtccagc	420
aacaagatca	tcaatcttgc	ccctgggaca	gtgagctcta	ccagcgcaga	cgcggtaaac	480
ggctcgcagt	tgtatgcgac	gaaccagaac	gtgtcgaaca	tcggaaacac	ggtgaacaac	540
atcaccaccg	gtgccggcat	catgtacttc	cacgtgaact	cgacgctggc	ggattcgacc	600
gcgaacggcg	tgaattctat	tgctatcggt	ggcgcgacca	gaacggacgc	gaacaattcg	660
atttcgatcg	gtacgggact	gacgcaagcc	tcaagcaata	caggggctat	cgcaattggt	720
cagaatgcga	gcatcaatgt	atacggcgcg	aatagtatcg	ctatcggcac	aaacagtgcg	780
acgggtggca	ttggcggtgc	gattgcgctc	ggcgagaacg	cctttgcaac	cggcggcaag	840
atggtggcgc	tcggctccgg	tgcgagtgcg	acgacggcta	attcgggtcg	gctagggtca	900
ggttcgacga	cgacggcgaa	tttgacagca	gcaggatata	accctggcag	cggcacgctt	960
gccggtacgt	cacaggctac	gaatggcgaa	gtgtcgggtg	gcaatgcagg	tgcaagcgtg	1020
cgtatcacta	acgttgccgg	cggttcggca	gccacggatg	cggtgaacgt	gagccagtgt	1080
caatcggaag	atgcaaaggt	gaacacgac	aacaacaacg	tgaacaacct	gagcggcagt	1140
gtcaccaaca	tcagcagcac	ggtgaacaac	atcaccaacg	gtggtggcat	caagtatttc	1200
cacgcgaact	cgacgcaggc	ggattcgctc	gccacgggca	cggtatgcag	ggcgatcggt	1260
ggcaatgccc	aggcgacggc	ggcgaaactc	gtggcgctgg	gtttgaactc	gacgagtaag	1320
ggaacgaacg	cgattgcact	gggcggggcc	gtggctgggg	ggagctacgc	tttcgcggca	1380
ggcagcctgg	cattggctgc	aactactggt	gacattgcgc	tgggttcac	ggcgacggct	1440
agcagcgcta	acagcaatgc	ttacgcaact	gcgctgggta	ccaacgcggt	ggcaaacgca	1500
accgatgcaa	ctgccattgg	cgaagggtgc	tcggcaacag	cagcatcctc	ggtagcgttg	1560
ggcgcgagat	ccaaaacgac	agcgaacctg	tcgacagcgg	gctataaccc	gggtacgggg	1620
acgttgctcg	gtactacccc	gacgggcgaa	gtgtcgggtg	gctcggcagg	caaggaacga	1680
cgcgtagcga	acgtggcagc	cggctcggca	gcgacggatg	cggtgaacgt	gagccagtgt	1740
atgtcggaag	acgcaaaggt	gaacacgac	aacaacaacg	tgaacaacct	gagcaacaac	1800
gtcacgaaca	tcgcgggcaa	tgtaaccaac	atcagcaaca	cggtgaacaa	catcaccaat	1860
ggtggtggca	tcaagtactt	ccacgtgaac	tcgacgctgg	cggattcttc	cgcgggggga	1920
acaaattcta	tagctatcgg	cggcggggct	actacgggga	atgttactgc	aggaacttca	1980
gacaatatat	ccatcggcac	caacgccaca	accaactatg	gcaaaaatat	tgccatcggc	2040
ggcaatgcgc	aggccttggg	aggcgcatat	gacggtggct	acaacactgc	gattggtgag	2100
aacgcgattg	caaagggaga	tggagcaggt	ggcttcggcg	gaggggggtg	ggggcagacc	2160
acggccattg	gcggtggttc	gcaggcattg	catgacaaca	ccacggcggt	cggttcaggc	2220
gcgatcgcaa	atgtggctaa	tgctactgct	ttgggtatgt	ctgccagcgc	gaccgctggg	2280
agtgcctatcg	cgctgggtca	gggggcagtg	gcgtcggcag	cgaactcggt	ggcactgggt	2340

tcggggttcga	cgacgacgnc	gaacctgtcg	gcagcggggtt	ataacccggg	tacgggtaca	2400
ttgtcgggca	tcgcttcggt	agccaatggc	gaagtgtcgg	tgggtgcagc	aggcaaggaa	2460
cgtcgcatca	ccaacgtggc	agccggctcg	gcagccacgg	atgcagtga	cgtgagccag	2520
ttgcaatcgg	aagatgcaaa	ggtgaacacg	atcaacaaca	acgtgaacaa	cctgagcggc	2580
agtgtcacca	acatcagcaa	cacggtgaac	aacatcacca	acggtggtgg	catcaagtat	2640
ttccacacga	aatcgacgct	ggccgattcg	tcggcgacgg	gtacggatgc	agtggcgatc	2700
ggcggcaatg	cccaggcgac	ggcggcgaa	tcggtagcac	tgggttcgaa	ctcgacgacg	2760
acagcgaacc	tgctggcagc	gggttataac	ccgggcacgg	gtgctgtgtc	tggcatcgct	2820
tcggcagcca	acggtgaagt	gtcgggtgggt	gcagcaggca	aggaacgccc	catcactaac	2880
gtagcagccg	gctcggcagc	cacggatgcg	gtgaacgtca	gccagctcca	gtcgggaagac	2940
gcaaagggtga	acacgatcag	caacaacgtg	aacaacctga	gcggcagcgt	caccaacatc	3000
agcagcacgg	tgaacaacat	caccaatggt	ggtggcatca	agtacttcca	cacgaactcg	3060
acgctggcgg	attcgaccgc	gaacggcgtg	aattctattg	ctatcgggtg	cgcgaccaga	3120
acggacgcga	acaattcgat	ttcgatcggt	acgggactga	cgcaagcctc	aagcaataca	3180
ggggctatcg	caattggtca	gaatgcgagc	atcaatgtat	acggcgcgaa	tagtatcgct	3240
atcggcacaa	acagtgcgac	gggtggcatt	ggcgggtgca	ttgctgctcg	cgagaacgcc	3300
tttgcaaccg	gcggcaagat	ggtggcgctc	ggctccgggtg	cgagtgcgac	gacgggcta	3360
tcggctcgcg	taggctcagg	ttcgacgacg	acggcgaatt	tgacagcagc	aggatacaac	3420
ccgggcagcg	gcacgcttgc	cggtagctca	caggctacga	atggcgaagt	gtcgggtggc	3480
aatgcagggtg	cagagcgctc	tatcactaac	ggtgctggcg	gctcggcagc	cacggacgcg	3540
gtgaacgtga	gccagttgca	gtcgggaagat	gcgaagggtga	acacgatcaa	caacaacgtg	3600
aacaacctga	gcaacaacgt	cacaaacatc	gcgggtaacg	tcaccaacat	cagcaacacg	3660
gtgaacaaca	tcaccaatgg	tggtggcatc	aagtatttcc	acacgaaatc	gacgctggcc	3720
gattcgctcg	cgacgggcac	ggatgcagtg	gcgatcggcg	gcaatgccca	ggcgacggcg	3780
gcgaactcgg	tagcactggg	ttcgaactcg	acgacgacag	cgaacctgtc	ggcagcgggc	3840
tacaacccgg	gcacgggtac	gctgtccggt	actaccccga	cgggcgaagt	gtcgggtggc	3900
tcggcaggca	aggaacgtcg	cgtgacgaac	gtggcagccg	gctcggcggc	gacggatgcg	3960
gtgaacgtga	gccagttgca	gtcggccatc	atcggcagca	ccgcgaacgc	ggtcgcctat	4020
gacgacggca	cgaaggccac	ggttacgctg	aagggcgcga	gcggcacgaa	gatcaccaac	4080
ctgacggcgg	gcaatctgag	cgcaacgagc	acggacgcgg	tgaacggctc	gcagttgtac	4140
gcgacgaacc	agaacgtgtc	gaacatcggt	aacacgggtga	acaacatcac	caacgggtgg	4200
ggcatcaagt	atttccacgc	gaactcgacg	caggcggatt	cgtcggccac	ggggtcgaac	4260
tcggctcgcg	tgggcgacag	ggcgtcgctc	cttggcggtt	cgtcggctcg	gatgggtgac	4320
ggcgcgacag	cagtgggcgc	ggcagagtatt	gcgattggta	acaatgcgca	gaacgtgacc	4380
gggtcgaaca	attcagttgc	cattggaggt	gattcgaagg	cgggcgacag	gtccgtttca	4440
ctgggcaacg	gtgcagatac	ctcgtgtctg	agctggggcg	ttgcagtcgg	taccaacgcg	4500
aacgttttctg	ctgcactggg	cacggcaatt	ggtgccgggg	ccaacgtgag	cggcgcgaat	4560
tcgacggcca	tcgggcgcgaa	cgcggtggcc	tctgcgacca	actcgggtgg	gctgggttcg	4620
aattcgacga	cgacggcgaa	cctgtcgget	gcgggttata	acccgggtac	gggtacgttg	4680
tcgggcatcg	cgtcggcggc	caatggcgaa	gtgtcggtcg	gtgcagcagg	caaggaaacgt	4740
cgcgtgacga	acgtggcagc	cggctcggca	gccacggatg	cgggtgaacgt	gagccagttg	4800
cagtcggaag	atgcgaaggt	gaacacgatc	aacaacaacg	tgaacaacct	gagcggcagt	4860
gtcaccaaca	tcagcagcac	ggtgaacaac	atcaccaacg	gtagcggcat	caagtacttc	4920
cacacgaact	cgacgttggc	ggattcgctc	gctggggggg	ccaatagcat	tgctatcggt	4980
ggcggggcgg	cgaccagtag	cagtgccggc	ctgagtga	acatggcgat	cggcaccaac	5040
gccaccgcaa	gctacggcaa	gaacatcgcc	atcggcggcg	gtgcgcaggc	tacagggtggc	5100
acgtacgacg	gcggctataa	cgtcgcactc	ggtgaaaacg	ctaattgccac	agcaggcacg	5160
aacgcctggg	gacacaatac	ggcgatcggt	gccaacaccg	taatcaatgg	cgtcaactcg	5220
gtagcgctcg	ggatctcggc	gacgacgagc	gggagcggca	gcatggcctt	tggctcggcg	5280
gcacaggcaa	gcgcggacta	tgcgattgca	agtggggcag	gcgccaatgc	atcggctgtg	5340
aattccgtgg	cgctgggttc	gaactcgacg	acgacggcca	acctgtcggc	agcgggttat	5400
aacccgggta	cgggtacgct	gtcgggcac	gcttcggtag	ccaatggcga	agtgtcgggtg	5460
ggctcggcag	gcaaggaaacg	tcgcgtgacc	aacgtggcag	ccggttcggc	agcgacggat	5520
gcggtgaacg	tcagccagct	ccagtcggaa	gacgccaagg	tgaacacgat	caacaataac	5580
gtgaacaacc	tgagcaacaa	cgtcagcaac	atcgcgggca	acgtcaccaa	catcagcaac	5640
acggtgaaca	acatcaccaa	cgggtggcggc	ggcatcaagt	acttccacgc	gaactcgaca	5700
ctcgccgatt	cgtcggcaac	gggcacggat	gcagtggcga	tcggcgggaa	tgcccaggcg	5760
acggcggcga	actcggtagc	actgggttca	aactcgacga	cgacggcaaa	cctgtcggca	5820
gcgggctaca	acccgggcac	gggtacgctg	tccggtagca	ccccgggtgg	cgaagtgtcg	5880
gtgggctcgg	caggcaagga	acgtcgcgtg	acaaacgtgg	cggccggctc	ggcggccacg	5940
gatgcgggtga	acgtgagcca	gttgagctcg	gccatcatcg	gcagcaccgc	gaatgcggtc	6000
gcctatgacg	acggcacgaa	ggccacgggtt	acgctgaagg	gcgcgagcgg	tacgaagatc	6060
accaacctga	cggcaggtaa	tctgagcgca	acgagcacgg	acgcggtgaa	cggctcgacg	6120
ttgtatgcga	cgaaccagaa	cgtgtcgaat	gtcggtaaca	cggtcagtaa	cctgagcaac	6180

aacgtcacga	acatcgcggg	taacgtcacc	aacatcagca	acacggtgaa	caacatcacc	6240
aatggtggtg	gcatcaagta	tttccacgcg	aactcgacgc	tcgccgattc	gtcggcgacg	6300
ggcacggatg	cagtggcgat	cggtggcaat	gcccaggcga	cggcagcgaa	ctcgggtggcg	6360
ctgggttcaa	actcgacgac	gacggcgaac	ctgtcggcag	cgggctataa	ccctggcacg	6420
ggtgcgttgt	ccgctacgac	cccgggtggg	gaagtgtcgg	tgggctcggc	aggcaaggaa	6480
cgtcgcgtga	cgaacgtggc	agccggctcg	gcagcgacgg	atgcagtga	cgtcagccag	6540
ttgatgtccg	aagatgccaa	ggtgaacacg	atcaacaaca	acgtgaacaa	cctgagcaac	6600
aacgtcagca	acatcgcggg	taacgtcacc	aacatcagca	atacgggtgaa	caacatcacc	6660
aacggtggca	gcggcatcaa	gtacttccac	gcgaactcga	cgctggcgga	ttcgtcggca	6720
acgggcggtg	acgcagtggc	gatcggcggc	aatgccagg	cgacggcagc	gaactcggta	6780
gcactgggtt	cgaactcgac	gacgacagcg	aacctgtcgg	cagcgggtta	taacccgggc	6840
acgggtgcgt	tgtctggcat	cgcttcggca	gccaacgggtg	aagtgtcgggt	gggtgcagca	6900
ggcaaggaa	gccgcatcac	taacgtagca	gccggctcgg	cagccacgga	tgcgggtgaac	6960
gtcagccagc	tccagtcgga	agacgcgaag	gtgaacacga	tcaacaacaa	cgtgaacaac	7020
ctgagcaaca	acgtcagcaa	catcgcgggc	aacgtcacca	acatcagcaa	tacgggtgaac	7080
aacatcacca	acgggtggcag	cggcatcaag	tacttccacg	cgaactcgac	actcgccgat	7140
tcgtcggcaa	cgggcacgga	tgcagtggcg	atcgggtggga	atgcaticggc	atcggcggca	7200
aactcgggtg	cgctggggtt	gaactcgacg	acgacggcga	acctgtcggc	agcgggatac	7260
aacccgggtt	cggcagcact	gtcgggcacg	gcctcggcag	ccaacggcga	agtgtcggtc	7320
ggtgcagcag	gcaaggaa	ccgcatcacg	aacgtagcag	ccggctcggc	agccacggat	7380
gcgggtgaacg	tgagccagct	ccagtcgga	gacgcgaagg	tgaacgctga	aggcgcggcc	7440
actgcggcag	cgctgggcg	cggttcgacc	tacaacacga	cgacgggtgc	gatcaccagt	7500
ccgacgtaca	tcgcaggcgg	caagacgttc	aacaatgttg	gcgatgtagt	cacgaacatc	7560
gacggccgtg	ttacgcagaa	ctcgacggac	atcacgaacc	tgactacgac	catcgacaac	7620
ggcacgatcg	gtctggtgca	gcaggctacg	ccgacgagca	cgattacgggt	cgcgaaggac	7680
acgggcgggc	cgacgggtgga	tttccggggc	acgggcaatg	caactcgcac	gttgacgggc	7740
atcacggcgg	gtgagttgag	cgcaacgagc	acggatgcgg	tgaacggctc	gcagttgtac	7800
gcgacgaacc	agaacgtgtc	gaacattgac	aacacgggtca	gtaacctgag	caacaacgtc	7860
acgaatatcg	cgggcaatgt	caccaacatc	agcaacacgg	tgaataacat	caccaacggt	7920
ggtggcgggca	tcaagtactt	ccacgcgaac	tcgacgctgg	cggattcgtc	ggcaacgggc	7980
gttgacgcag	tggcgatcgg	cggaatgcc	caggcgacgg	cagcgaactc	ggtagcactg	8040
ggttcgaact	cgacgacgac	agcgaacctg	tcggcagcgg	gctacaacc	gggcacgggc	8100
acgttgtctg	gcatcgcttc	ggcagccaac	ggtgaagtgt	cggtcgggtg	agcaggcaag	8160
gagcgcccg	tgacgaacgt	agcagccggc	tcggcagcca	cggacgcgggt	gaacgtgagc	8220
cagttgcaat	cggaagatgc	caagggtgaac	acgatcaaca	acaacgtgaa	caacctgagc	8280
aacaacgtca	gcaacatcgc	gggcaatgtc	acgaacatca	gcaacacgggt	gaacaacatc	8340
accaacgggtg	gcggcgccat	caagtacttc	cacgcgaact	cgacgctggc	ggattcgtcg	8400
gcgacggggca	ccaacagcct	ggcgccggga	ccggcagcgg	tgccatccgc	cactgacgca	8460
gtcgcactgg	gcaacggcgc	gaaggcaacc	aacgcccggcg	cggtggcact	cggcgcagggt	8520
tcgacgacaa	cgaccgcgggt	ggcaacctcc	ggcacgacga	ttggcgccat	cacctacacg	8580
ttcgaggcg	tcgctccgtc	gagcacgggtg	agcgtgggtg	cggcgggtag	cgagcgacg	8640
atcacgaacg	tggcggctgg	ccgcctgagc	gcgacgagca	cggacgcgggt	caacggcagc	8700
gaactgtttg	caaccaacca	gcagggtgacg	cgaaacaccg	cggacatcac	caacctgacg	8760
aacaacatga	acatcggttc	ggtgggtctg	gtgcagcagg	acgcgacgac	acgcaccatc	8820
acggtcgcga	aggccaccga	cggtacgcgg	gtcgacttca	cgggcacggg	gggcgcgcgt	8880
caattgacgg	gcgtggccgc	aggcgcagtg	aacgcgacga	gcgtggatgc	ggtgaacgggt	8940
tcgcagctct	acgggtgtgtc	gcagagcggtg	gcggatgcga	tcggcggtgg	ctcgaccgtg	9000
aacacggatg	gtcccatctc	ggccccgacc	tacgttgttg	acggcacgac	cgtccacaat	9060
gcgggcgacg	cgatcagcaa	cctcgacaac	cgtgtgacgc	agaacaccac	cgacatcagc	9120
acgatcaaca	acacgctgaa	cagcatcacc	acgggtgcgg	gcgtcaagta	cgtgcatgtg	9180
aactcgaccc	tgcccgactc	gctggcgaa	ggtgcggagt	cgggtggcgt	cggcggtaac	9240
gcgcaatcgc	aggcggcgaa	ctcgggtggca	ttgggttcga	actcgggtggc	ggatcgtgcc	9300
aacacgggtg	cggtgggctg	ggctgggtgcg	gagcgtcaga	tcaccaacgt	ggcgccgggt	9360
acggcgga	cggtgcgggt	gaacgtcgcg	cagttgaagg	cgtcgggtgt	gatcaatac	9420
gatggcacga	ccaacgccgc	cgtcacgtac	gaccacaacg	cggacggctc	ggccaactac	9480
aacagcgtca	cgatgggtaa	cggtgtagcg	ggcggcacga	cgatccacaa	cgtggcgggca	9540
ggctcggctg	ccgacgacgc	ggtcaacgtc	agccagatga	acgcggcgat	ctccagcgtc	9600
tcgaacatca	tcggctcggc	gggtaatccg	ctgttcacag	ccgacggcaa	ccgtgacacg	9660
gaagcccgcg	tcgccagcgg	cacgcacgtc	acggcaatgg	gcgcgaacgc	gaaggcaagc	9720
gcggccaatt	cggtggcgct	gggtgcgaac	tcgggtggcg	accgtgagaa	tacgggtgtcg	9780
gtgggctcgg	cgggcaacga	acgccagggtc	accaatgtcg	cggccgggtac	ggccaccacc	9840
gacgccgtca	acgtcggcca	gttgaaccag	gcgatcggcg	catcgatcgg	caatctgccg	9900
gccggcatgt	cggcgaaggga	ctacaccgac	cagcagatca	acgcgggtgca	gaacggcggtg	9960
aaccagggttg	cgaagaacgc	gtatgcagggt	atcgcgggcg	ctacggcgct	gacgatgatt	10020

ccggacgtcg	atcagggcaa	gacgatcgcg	gtcgggtgtcg	gcggcggctc	gtataaggggt	10080
tcgcaggctg	tggcgctcgg	catctcggca	cgtatcaccc	agaacctgaa	gatgaaggcc	10140
ggcgcgggta	cgagctcgca	aggcacgacg	gtgggccttg	gtgcttccta	ccagtggtaa	10200

<210> 30
 <211> 1734
 <212> DNA
 <213> Escherichia coli

<400>	30					
atgctgatcc	agcagaacag	cgaagtcatc	aatcagcttg	ccggtaacac	cagtgaacc	60
tacatcgaag	aaaatggtgc	aagtattaac	tatgtgcgta	ccaatgacac	cggtttaacc	120
ttcaccgatg	ccagcgcagc	aggtattggc	tctaccgctg	tggggataaa	cactggtgcc	180
aaaggcgata	acagcgtggc	catgggttat	aactcttttg	ccgaaggcca	tagtagcgtg	240
gccatcggtc	agggcagcta	cagcggcggt	gagacgagta	ttgcgctggg	tagcgaatcc	300
gtctccagcc	gcgtgattgt	taaaggttct	cgtaaacacga	gcgtatcgga	agaagggtgt	360
gtgattggtt	atgacaccac	ggatggcgaa	ctgcttgggc	cattgtcgat	cggtgatgat	420
ggtaaataatc	gtcaaatacat	caacgtcgcg	gatgggttctg	aagcccatga	cgctgttact	480
gttcgccagt	tgcaaaacgc	cattgggtgca	gtagcaacca	caccaaccaa	atactatcac	540
gctaactcaa	cggctgaaga	ctcactggca	gtcgggtgaag	actcgcctggc	aatgggcgcg	600
aaaaccatcg	ttaatggtaa	tgccgggtatt	ggatcgggcc	tgaacacttt	agttctggct	660
gatgcgatca	acgggtattgc	tatcggttct	aacgcacgcg	caaatcatgc	cgacagcatt	720
gctatgggta	atgggttctca	gactactcgt	gggtgcgcaga	ccaactacac	tgccataaac	780
atggatgcac	cgcagaactc	tgtgggtgag	ttctctgtcg	gcagtgaaga	cggtcaacgt	840
cagatcacca	acgtcgcagc	ggggtcggcg	gataccgatg	cggttaacgt	gggtcagttg	900
aaagtaacgg	acgcgcaggt	ttcccagaat	acccagagca	ttactaacct	gaacactcag	960
gtcactaatc	tgataactcg	cgtgaccaat	atagaaaacg	gcattggcga	tatcgtaacc	1020
accggtagca	ccaaataactt	caagaccaac	accgatggcg	tagatgccaa	cgcgcagggt	1080
aaagacagtg	ttgcgattgg	ttctgggttcc	attgctgccc	ctgacaacag	cgctcgcgctg	1140
ggtacaggct	ccgtggccaa	cgaagaaaat	accatctctg	tgggttcttc	taccaaccag	1200
cgccgtatca	ccaacgttgc	tgccgggtgt	aatgccaccg	atgcgggttaa	cgtttcgcaa	1260
ctgaagtctt	ctgaagcagg	cggcggttcgc	tacgacacca	aagctgatgg	ctctatcgac	1320
tacagcaaca	tactctcgg	tgggtggtaac	ggcggtagca	ctcgcatcag	caacgtttct	1380
gctggcgtga	ataacaacga	cgcgggtgaac	tacgcgcagt	tgaagcaaag	tgtgcaggaa	1440
acgaagcaat	acaccgatca	gcgcagtgggt	gagatggata	acaaactgtc	caaaactgaa	1500
agcaagctga	gtgggtggtat	cgcttctgca	atggcgatga	ccggctctgcc	gcaggcttac	1560
acgccgggtg	ccagcatggc	gtctattgggt	ggcgggtactt	acaacgggtga	atcggctggt	1620
gcttttaggtg	tgtcgatgggt	gagcgccaat	ggtcggtggg	tctacaaatt	acaaggtagt	1680
accaatagcc	agggtgaata	ctccgcccga	ctcgggtgccg	gtattcagtg	gtaa	1734

<210> 31
 <211> 4663
 <212> DNA
 <213> Shigella sp

<400>	31					
atgaacaaaa	tattttaaagt	tatctggaac	cctgcgacag	ggaattatac	tgttaccagc	60
gaaacggcaa	aaagccgtgg	caagaaatct	gggcgcagta	agctgttaat	ttctgcgctg	120
gttgcgggtg	gaatgttgtc	gtcgtttggg	gcattggcga	atgccgggaa	tgacaacggt	180
cagggtgttg	attacggtag	tggatcagct	ggcgcagcgt	gggttgctat	aggcaaaggg	240
gcgaaagcaa	atacttttat	gaacaccagt	ggttccagta	ctgctgtggg	ttatgacgct	300
atagctgaag	gccaatatag	ctctgccatc	gggtcaaaaa	cccatgcgat	tgggtggtgca	360
tcaatggcct	ttgggggttag	tgcaatatca	gaaggcgata	gaagtatagc	actgggtgcc	420
tcttcgtatt	cattgggcca	atactcaatg	gccctcggcc	gttattcaaa	agcattgggt	480
aaattgtcta	ttgctatggg	ggactcttcc	aaagcggaag	gagcaaacgc	cattgccctg	540
gggcgtagca	gtgtagctag	cggtactgac	agcctcgcac	ttggcagaca	atcacttgcc	600
agcgcagcga	acgctattgc	gatagggtgct	gagaccgaag	ccgctgaaaa	tgcaactgct	660
attggcaata	atgcgaaggc	aaaagggact	aatagcatgg	caatgggggt	cggaagcctt	720
gccgataaag	tcaatactat	cgcattagga	aatggcagcc	aggctctggc	agataatgca	780
atcgccatag	gccagggcaa	caaagctgat	ggcgtggatg	ccatcgctct	gggtaatggt	840
agccagtcga	gaggcttaaa	caccattgcc	ttaggcacag	ccagtaatgc	aactggtgat	900
aagagtcttg	cgcttggtag	taatagcagt	gccaacggta	ttaactctgt	cgcgctgggc	960
gcagattcca	ttgcggattt	agacaatacc	gtctctgtcg	gcaatagtcc	attaaaacgc	1020
aagatcgтта	atgtgaaaaa	tggcgcgatc	aagtctgaca	gttacgatgc	cattaatggt	1080

tcacagcttt	atgccattag	cgactcggta	gcaaaaaagg	cttggaggag	gggctgcagt	1140
agatgttgat	gacggtactg	ttacagcacc	aacctacaat	ttaaaaaatg	gtagcaaaaa	1200
taacgtaggg	gctgcgctcg	ctgtacttga	tgaaaacacc	ctgcaatggg	accaaaccac	1260
aggcaaatac	agcgctgctc	atggtactag	tagcccaact	gccagcgtaa	tcaccgatgt	1320
tgcggatggc	acgatttcag	cctccagtaa	ggatgcggtt	aacggttccc	aactgaaagc	1380
taccaatgac	gatgtcgaag	ccaacaccac	caatatcacc	aacctgacgg	attccgttgg	1440
tgaccttcag	gctgatgccc	tgctctggaa	cgaaactaaa	aaggcattca	gtgcagctca	1500
cggccaggat	accaccagca	aaatcaccaa	cgtaaagat	gccgacctga	cggctgacag	1560
cactgatgct	gttaacggct	ctcagctgaa	aaccaccaac	gatgctgtgg	cgacgaatac	1620
caccaatata	gccaaataca	cttccaatat	tgccactaac	accaccaaca	tctctaacct	1680
gactgagacg	gtgactaatc	ttggtgagga	tgcgctgaaa	tgggataagg	acaatgggtg	1740
attcacggca	gctcatggca	ccgagaccac	cagcaaaata	accaacgtta	aagatggcga	1800
cctgacgact	ggcagcacgg	atgccgttaa	cggctctcag	ctgaaaacca	ccaacgatgc	1860
cgtggcgacg	aataccacca	atatcgccac	taacaccacc	aacatctcta	atctgactga	1920
gacggtgact	aatcttgggtg	aggatgcgct	gaaatgggat	aaggacaatg	gtgtcttcac	1980
tgacgctcat	ggcaacaata	ccgccagcaa	aatcaccaat	atcctggacg	gcacagtcac	2040
tgcaaccagt	tccgatgcc	ttaacggtag	ccagctttat	gacttaagca	gcaatatcgc	2100
cacctacttc	ggcggcaatg	cttctgtgaa	tactgacggg	gtgtttaccg	gtccaacct	2160
caaaatcggg	gaaacaaatt	attataacgt	cggcgatgca	ctggctgcga	ttactcctc	2220
atttagcacg	tctctcggcg	atgctctgct	ttgggatgcc	accgcaggta	aattcagtgc	2280
caaacacggg	actaatgggtg	acgcaagcgt	gatcactgat	gtcgcagatg	gtgaaatttc	2340
agactccagt	tctgacgcag	taaacggctc	acaactccac	ggcgtgagca	gttatgttgt	2400
tgatgcgctg	gggggtgggtg	ccgaagtcaa	tgacagcggc	accatcactg	cgccgacgta	2460
caccattgct	aatgctgatt	acgataatgt	cgggtgatgcc	ctgaatgcta	tcgataccac	2520
tcctgacgac	gctctgctct	gggatgcgga	cgccggtgaa	aatggtgcat	ttagcgccgc	2580
tcacggaaaa	gataaaactg	ccagtgtaat	cactaacgtc	gctaacgggtg	caatctctgc	2640
tgccagcagc	gacgcgatta	acggctcaca	actctatacc	accaataagt	acatcgctga	2700
tgcgctgggt	ggtgacgcag	aagtcaacgc	tgacggcacc	atcacgcac	cgacttacac	2760
cattgcgaac	gccgagtaca	acaacgtcgg	tgacgccctg	gatgcgcttg	atgataacgc	2820
cctgctgtgg	gataagactg	ccaatggcgg	tgctggagcc	tacaatgcca	gccatgacgg	2880
taaagccagc	atcatcacta	atgtcgctaa	tggcagtatt	agtgaggaca	gtaccgatgc	2940
agtgaacggg	tctcagttga	atgcgacgaa	tatgatgatt	gagcagaaca	cccaaattat	3000
caatcagctc	gctggtaaca	ccgacgcaac	ctatatcgaa	gaaaatggcg	ctggtatcaa	3060
ctacgttcgt	actaacgaca	acgatttagc	ctttaacgat	gcaagcgctt	ctggtgtcgg	3120
cgctacagct	gtaggttata	acgctgtcgc	gtctgggtgcc	agcagcgtag	ccattgggtca	3180
gaacagcagc	agcaccgttg	ataccggtat	tgcgctgggt	agcagctccg	tttccagccg	3240
tgtgattgcc	aaagggttctc	gtgacactag	cgtaacggaa	aatggcggtg	tgattgggtta	3300
tgacaccact	gacggcgaac	tgctaggtgc	attgtcaatt	ggtgatgacg	gtaaataaccg	3360
ccaaatcatc	aacgtagctg	atggttcaga	agcccatgac	gccgttacgg	ttcgccagtt	3420
gcagaacgct	attggagcgg	tcgccactac	gccaaccaag	tactttcacg	ccaactcaac	3480
ggcagaagac	tcactggccg	ttggtgaaga	ctcgctggca	atgggtgcga	aaactgtcgt	3540
taatggtaat	gcagggtattg	gtatcggttt	gaacactctg	gttctggctg	atgcgatcaa	3600
cggcattgct	atcggcagta	acgcacgcgc	aaaccatgca	aacagtatcg	caatgggtaa	3660
cggttctcag	accacccgtg	gtgcacagac	tggttacacc	gcctacaaca	tggaacgcacc	3720
gcagaactct	gtaggtgagt	tttctgtcgg	tagtgaagac	ggtcaacgtc	agatcacaaa	3780
cgtcgcagct	ggttcagcgg	ataccgatgc	ggttaacgtg	ggtcagttga	aagtcactga	3840
tgagcgcgta	gcgcaaaata	cccagagcat	tactaacctg	aacaatcagg	tcactaatct	3900
ggatactcgc	gttactaata	tcgaaaacgg	tattggcgac	attgtcacca	ccggtagcac	3960
caagtacttc	aagaccaaca	ccgatggcgt	agatgccaac	gcccagggtg	aagatagcgt	4020
tgctattggg	tctggttcca	ttgctgccgc	tgacaacagc	gtcgcactgg	gtaccggttc	4080
cgttgacagag	gaagaaaata	caatctctgt	aggttcttct	actaaccaac	gccggatcac	4140
caacgtagct	gccagtgtta	atgccaccga	tgcggttaac	gtgtcgcagc	tgaaatcttc	4200
tgaagcaggc	ggagtgcgct	acgacacca	agctgatggg	tctatcgact	atagcaatat	4260
caccctcggg	ggtggcaacg	gcagtacgac	tcgtatcagc	aacgtctccg	ctggcgtaaa	4320
caacaacgac	gcggtgaact	acgcgcagtt	gaagcaaagc	gcgcaggaaa	cgaagcaata	4380
caccgatcag	cggatgggtg	agatggataa	caaactgtct	aaaactgaaa	gcaagttgag	4440
cgggtggatc	gcttctgcaa	tggcaatgac	cggctctgccg	caggcttata	caccgggtgc	4500
cagcatgggt	tctattgggtg	gcggtactta	caacgggtgaa	tcggcagttg	ctttaggtgt	4560
atcgatgggtg	agcgccaatg	gtcgttgggt	ctacaaatta	caaggtagta	ccaatagcca	4620
gggtgaatac	tccgccgcac	tcggtgccgg	tattcagttg	ttaa		4663

<210> 32
 <211> 684
 <212> DNA

<213> Brucella melitensis

<400> 32

atgtcttttt	ttaaaaaaaaa	tatatcgata	acagccatgg	gtggcttgat	gttgctgctt	60
gcagtcgacg	ctgcgaaggc	ggaggaaaat	gtttcgcagg	tgaaacttcc	tcctgttttt	120
gtttttgagc	ttgttgaaaa	ccaggggctg	gccaatattg	ctctgattcg	acctcgagtg	180
atagcgccag	acaacaacct	acgtcctggg	ggcattgtgt	ctgggatcgc	tggctttttg	240
actctcgggc	aggagaaccg	caacctaat	agtgaaaata	ggcaagttat	taataacaat	300
acgactgcca	ttggccagaa	tcgtacctcg	attagtagca	atgccaaagg	cggtgcccgc	360
aatagggctg	ctatcagaca	gaatagtgt	gcgatttccg	ctcttgcca	gcgagttgac	420
gggttgcaag	gtcagatcaa	cagcgcccgg	aaagaggcac	gtgccggagc	tgcaaatgcc	480
gctgctcttt	cggggctaag	atatgataac	cgtccaggca	aggtgtcaat	cgctaccggt	540
gttggcggct	ttaaaggtag	caccgctttg	gctgctggta	tcggttacac	aagcaagaac	600
gaaaacgctc	gttataacgt	gagtgtagct	tacaacgaag	ctggcacatc	ctggaatgca	660
ggtgcaagct	ttacgcttaa	ctaa				684

<210> 33

<211> 936

<212> DNA

<213> Brucella suis

<400> 33

atgtcttttt	ttaaaaaaaaa	tatatcgata	acagccatgg	gtggcttgat	gttgctgctt	60
gcagtcgacg	ctgcgaaggc	ggaggaaaat	gtttcgcagg	tgaaacttcc	tcctgttttt	120
gtttttgagc	ttgttgaaaa	ccaggggctg	gccaatattg	ctctgattcg	acctcgagtg	180
atagcgccag	acaacaacct	acgtcctggg	ggcatcgtgt	ctgggatcgc	tggcttctctg	240
actctcgggc	aggagaaccg	caacctaat	agtgaaaata	ggcaagttat	taataacaat	300
acgactgcca	ttggccagaa	cagcgatcgg	atcgacgcca	atgccaaagg	tggtgcccgc	360
aatagggctg	ccattggcca	gaacagcggc	cggatcgacg	ccaatgccaa	gggcgttgcc	420
gacaacaagg	ctgccattgg	ccgaaacagc	ggtcggatcg	acgccaatgc	caagggcggt	480
gccgacaaca	agactgccat	tggtcgaaac	agtggtcgga	tcgataccaa	tgccaaagg	540
gttgccgaca	atagggctgc	catcagccaa	aaccgcggtc	gcatcaatgc	taacgcagca	600
ggtgttgcta	gcaatagggc	tgctatcaga	cagaatagt	ctgcgatttc	cgctcttggc	660
cagcgagttg	acgggttgca	aggtcagatc	aacagcgccc	ggaaagaggc	acgtgcccga	720
gctgcaaatg	ccgctgctct	ttcggggcta	agatatgata	accgtccagg	caaggtgtca	780
atcgctaccg	gtgttggcgg	ctttaaagg	agcaccgctt	tggctgctgg	tatcggttac	840
acaagcaaga	acgaaaacgc	tcgtttataac	gtgagtgtag	cttacaacga	agctggcaca	900
tcctggaatg	cagggtgcaag	ctttacgctt	aactaa			936

<210> 34

<211> 3930

<212> DNA

<213> Ralstonia solanacearum

<400> 34

gtggttttca	gcgccatgcc	gcaatacgct	tgcgcagaaa	tggtgctgca	aaacgatccg	60
ggaacgaatt	gtggaagcgt	gggtgatgca	tatgcctggg	cgcgaggcga	tgggtattcg	120
ggttgtaagg	tcggttacga	agccgcaaaa	aatttgga	agggcacagc	attcggaat	180
agcctgggtc	aactatcgcc	tggtacgaac	attctcgtct	acgggtcgac	gctccgtgct	240
ggtatgaatg	acgaagtgc	acccctcgat	tcgatgaata	tcggtggcca	tctcgacgta	300
tggggagcca	gcggttttca	cggcggtgtc	gatatgaata	attccgccat	caaaaacctt	360
gctgacggca	cgctgtcggc	caccagcacc	gaggcgggtg	ctggcaggca	actgaacgcc	420
accaacacga	acatcaccaa	tctgcagaac	agcatcaaga	gcatcagcag	ttcggcgagc	480
ctggtgcagc	agtcggccgc	gggcaaggac	atcacagtgg	ccaaggacct	ggacggtgac	540
gcggtggact	tcagcggcaa	gaagctgagt	gacagcacga	cgttttcgcg	caagctgacg	600
ggtgtggcgg	aggggacggt	gtcggcgacg	agcacggatg	cggtgagcgg	caagcaactc	660
tatacgacca	accagaacct	gagcacgacc	aaccagaatc	tggcggacac	gaacaagagc	720
ctggccgaga	cgaacaagaa	cgtgtcggcg	accacgacca	acatcacgaa	cctgcagaac	780
accatcaaga	acatcagcgg	cggctcggcg	ggtctggtgc	agcaatcggc	cgcgggcaag	840
gacatcacgg	tggccaagga	cctggacggt	gaggcgggtg	acttcagcgg	caagaagctg	900
agcgacagca	cgacgttctc	gcgcaagctg	acgggtgtgg	cggaggggac	gctgtcggcg	960
acgagcacgg	atgcggtgag	cggcaagcag	ctctatacga	cgaaccagaa	tctggcgagt	1020
accaacaagg	acctggccaa	taccaacacg	cgcctgacga	cggccgaggg	caatctgtcg	1080
tcgaacacga	cgagcatcac	gaacctgcag	aacaccatca	agaacatcag	cggcggtctg	1140

gcgggtcttg	tgcagcaatc	ggctgcgggc	aaggacatca	ccgtggccaa	ggacctggac	1200
ggtgacgcgg	tggacttcag	cggcaagaag	ctgagcgaca	gcacgacgtt	ctcgcgcaag	1260
ctgacgggtg	ttgcggaggg	gacgttgtcg	gcgacgagta	ccgatgcggt	gagcggcagg	1320
cagctctata	cgaccaacca	gaacctgagc	acgacgaacc	agaatctggc	ggacacgaac	1380
aagagccttg	ccgagacgaa	caagaacgtg	tcggcgacca	cgaccaacat	cacgaacctg	1440
cagaacacgg	tgaacaacat	cagcagcggg	tcggcgggtc	tgggtgcagca	atcggcagcg	1500
ggcaaggaca	tcacagtggc	caaggacctg	gacggtgacg	cgggtggactt	cagcggcaag	1560
aagctgagtg	acagcacgac	gttctcgcgc	aagctgacgg	gtgtggcgga	ggggacgctg	1620
tcggcgacga	gcacggatgc	ggtgagcggc	aagcagctct	atacgacca	ccagaacctg	1680
agcacgacca	accagaatct	ggcggacacg	aacaagagcc	tggccgagac	gaacaagaac	1740
gtgtcggcga	ccacgacca	catcacgaac	ctgcagaaca	cgggtgaaca	catcagcagc	1800
ggttcggcgg	gtctggtgca	gcagtcggcc	gcgggcaagg	acatcacggt	ggccaagaac	1860
ctggacgggtg	acgcggtgga	cttcagcggc	aagaagctga	gtgacagcac	gacgttttcg	1920
cgcaagctga	cgggtgtggc	ggaggggacg	ctgtcggcga	cgagcacgga	tgcggtgagc	1980
ggcaagcagc	tctatacgac	caaccagaat	ctggcgagta	ccaacaagga	cctggccaat	2040
accaacacgc	gcctgacgac	ggccgagggc	aatctgtcgt	cgaacacgac	gagcatcacg	2100
aacctgcaga	acaccatcaa	gaacatcagc	ggcggctcgg	cgggtcttgt	gcagcaatcg	2160
gctgcgggca	aggacatcac	cgtggccaag	gacctggacg	gtgacgcggt	ggacttcagc	2220
ggcaagaacc	tgagcgacag	cacgacgttc	tcgcgcaagc	tgacgggtgt	tgcggagggg	2280
acgttgtcgg	cgacgagtac	cgatgcgggtg	agcggcaagc	agctctatac	gaccaaccag	2340
aacctgagca	cgacgaacca	gaatctggcg	gacacgaaca	agagcctggc	caagacgaac	2400
aacaacgtgt	cggcgaccac	gaccaacatc	acgaacctgc	agaacacggt	gaacaacatc	2460
agcagcgggt	cggcggggtct	ggtgcagcag	tcggcagcgg	gcaaggacat	tacggtggcc	2520
aaggacctgg	acggtgacgc	ggtggacttc	agcggcaaga	agctgagcga	cagcacgacg	2580
ttctcgcgca	agctgacggg	tgtggcgag	gggacgctgt	cggcgacgag	cacggatgcg	2640
gtgagcggca	agcagctcta	tgcgacgaac	cagaatgtgt	cgaagtgtgc	ggcgaacgtc	2700
acggacgtga	gtgatagcgt	caccaacatc	aagaacacga	tgaacaccat	cgtgaacggc	2760
ggcgggctca	agtacttcca	cgcgaactcg	acgctggacg	atgcgcaggc	gatgggcctc	2820
gagtcgatcg	cgttcggcgg	cgcagccgtc	gcggccggta	tgaactcgat	ggcgaatggc	2880
ggcaatgccc	gggcggtggc	gggcaacgct	gtggccttgg	gcgcgggttc	ggtggcggac	2940
cgcgcgaaaca	cgggtgtcgg	gggctcggcg	ggcaaggagc	gccagatcac	caacgtggcg	3000
gccggtacgg	cggacacgga	tgccgtgaac	ggtgcccagc	tgaaggcggc	cggcatcatc	3060
aacggcagcg	gcaggacca	cgccacgggtg	acgtacggca	ccaacgcaga	cggctcggcg	3120
gactacggca	acgtgacgct	gggcggcggc	aacgcgcggg	ccggcacggc	gatccacaac	3180
gtcgcgggccg	gcacggccga	gaccgacgcg	gtgaacgtca	ggcagatgaa	cgcgccattt	3240
gccagcgtgc	agaaggtgag	caacaccaac	gacccgatgt	tcgcggcgga	tggcgaccgc	3300
gctgtcaagc	gcgcgagcgc	caagggcacg	catgccacgg	cgatgggtgc	cgcgccagc	3360
gcgggcgggc	accagtcggt	cgcgacgggc	cacaacgcgc	agtcgggccc	cgacagctcg	3420
gtcgcgatgg	gcgcgaatgc	gaaggcgacg	gcgaatcatg	cggttgccgt	gggctcgggt	3480
tcggtagcga	accgcgcgaa	cacgatgtcg	gtgggctcgg	cgggcagcga	gcgccagatc	3540
accaatgttg	cggccggtgt	gcagggtacc	gatgcggtca	acgtgagcca	gctgagccag	3600
gcggtctatg	cggccgtcgg	cgatctgccg	gcgggcacga	cggccaggca	gtacacggat	3660
gagcagatcg	gcatggtgcg	gcaggggatc	agccaggtgg	cgcgcggcgc	ttacagcggg	3720
atcgcgggcg	cgaccgcgct	gacgatgatt	ccggacgtcg	atcagggcaa	gtcgatcgcg	3780
atcggtatcg	gcagcgcgac	ctacaagggc	tatcaggcgg	ttgcgctggg	cgcctcggca	3840
cgcatctcgc	acaacctgaa	ggccaagatg	ggcgtgggct	acagcagcga	aggcacgacg	3900
gtcggcatgg	gcgcgctcgt	tcagtggtaa				3930

<210> 35
 <211> 3876
 <212> DNA
 <213> Sinorhizobium meliloti

<400> 35						
gtggcgctgg	gacgccaatc	ggtctcggcc	ggcagcgggt	cacttgcatt	cggtaacggt	60
agttacgcga	attcaaacgg	atcggttgcc	atcgggcagt	ctgcatacgc	ggccaatggt	120
cgggcaatcg	caatcggtgg	agatgatgcc	ttcgcttggc	gagaggccga	gcagaccaag	180
gccgggggct	cccagtcgat	cgccatgggc	gtgcgtgcgc	gtacgaaatc	gctggtagtc	240
gacgacccgg	atacggtggc	caacgaagcg	gacccggggc	gcgcgtctga	tgccattgca	300
atcggtacgg	atgcacaggc	caatggcgac	cggctctctc	ccatcggcag	acagaatcag	360
gccggcaatg	agcaatccat	cggcatcggc	gcgggcaaca	cggcaacagg	caaactctcg	420
atcggcacgc	gcagcagcaa	cgtggccagc	ggcgagcaat	ccctaagcct	cggcgccggc	480
aacaatgccc	tggggcaggg	ctccatcagc	atcggtaccg	aaaccacagc	cggcggtctc	540
cggtcgatcg	ctttcggcgt	gcgcgcgagc	acgaaagaag	ccaatctaga	tattccggat	600

gacgtggccg	cgatcgacgc	catcgctatc	ggtaccaata	ccaaggccaa	cggcgaccgg	660
tccgtcagca	tcggaacggg	cagtcaagcc	agcagcggag	ccgtcagtat	tggcgatgca	720
gccaaaggctg	tgggtgacaa	atccgtcagt	atcggtagcg	aaagctgggc	cgatggcgac	780
gaatcgggtca	gcatcggcct	cgtcaacaac	gccgggtttg	aagggaatga	ccgaatcaaa	840
ggcgggcaaa	cctctgtcag	cctgggagcc	ttcaatcagt	cgccgggcat	cgaggccatt	900
gctatcgggtg	ccagaaacga	agccaatgcg	gatcggtcga	ttgcaatcgg	ctcgcgtgcg	960
aaaacgaagg	ccgccgatcc	ggcgcaggcg	gacggcgggtg	cgcgcgacgc	cgtcgctata	1020
ggcacggatg	cgctggccaa	cgacgaccgg	tccatcagca	taggctggaa	tagcagtacc	1080
tccctgaacg	attccatcag	catcgggtacc	cgagccacgt	cgggatcggc	gggcatatc	1140
atgatcggca	caggttcagg	gactgggttcc	acctccggtc	agaacaatgt	cgccctcggc	1200
gttgcgggcca	gtcagaagggt	gaagggggtcg	tcaaacatag	cgatcggcga	ttcggcgggc	1260
ggttcccggg	aaggcgataa	caacgtcgcc	ataggcacca	atgcgggaat	ccagttttcc	1320
gagagcgaac	atgagaccgc	cgtgcgcgcc	gacctcgtgg	tcagtgacgc	ggtgagcatc	1380
ggcaatgagg	cgctggcgag	cgccgatgaa	gccatcgcaa	tcggcaccgg	cgccgtggct	1440
tccggtttga	agtccatcag	catcggcgctc	ggaaataaccg	tcagcggcgc	ttcgagcggc	1500
gccatcggcg	atccgaccga	tatcaccgggt	accggctcct	actcgtggg	caacgacaac	1560
accatcgccg	ccgacaacgc	cggcaccttc	ggcaacgaca	acacattggc	ggatgccgcc	1620
gatggcagcc	gcgtcatcgg	caacggcaac	aatatcgatg	tgtccgatgc	cttcgtgctc	1680
ggcaatgggtg	ccgacgtcac	cgaagtcggc	ggcgtggcgc	tgggttccgg	ctcggtttcg	1740
gatacgggtg	ccgacgtggc	gggctatgtg	ccgggcgggg	cctcgacggc	cgaccaaacc	1800
gccatcgagg	cgacgcagag	cacgcgcggc	gcggctcgccg	tcggcaatcc	ggacgccgaa	1860
accggcgtct	accgccagat	cacagggtgtc	gccgcccggca	cggccgactc	cgatgccgcc	1920
aacgtggccc	agctcaaadc	ggtcgagacg	atcgccaaga	caggctggaa	gctcacgacg	1980
gacagcggca	gcatcgacgg	catcggggccg	ggcgacgagt	tggctcctca	aggcggcgac	2040
ggcaatatcg	tgatcagcaa	tcagatcttg	agcaacgacg	tgagcatcga	tctggccgat	2100
gagatcgagg	tgaacaggggt	gacggcgaga	gatcccagaca	cgggtgcatc	cacgggtgctg	2160
gacgagaacg	gcctgagctt	cacgacgcag	gacgcgaacg	gggaggacac	ggcgctcggc	2220
ccgcgcgtga	cggcgggcg	catccaagcg	gccggcaaaa	tcaccaatgt	cgctgcgggc	2280
gaggccgaca	ccgacgcgggt	gaacttttcc	cagctcaggc	aagtcgagac	cgcatcgggc	2340
aataccgacc	agcggggcggt	caaatatgac	tggaccgacg	ccaatacgaa	tggcgtgatc	2400
gatgaggggcg	aactcaacct	cgatagcggtg	acccttgccg	ggggcatggg	cggcaccagg	2460
atctccaatc	ttgcgcccgg	cgccttgagc	gcggcatcga	ccgatgccgt	caacggcagc	2520
cagctcttctg	ggcttcgcag	ccgcgtatcc	aacgtggccg	tcgccctggg	cgggggagcc	2580
gcctatgacc	ctgtcaagga	tgagtggatc	gccccgaaat	acacgatcgg	cggcaccgac	2640
tacagcaatg	tcggcgacgc	gctggcgggc	gtgggcgggca	cggccgggtg	cggctggagc	2700
ctctcggcgc	agggtgcgaa	cgcgctccaat	gtcgcgcggg	gcgagacgggt	ggatcttcgc	2760
agcggcgacg	gcaatatcgt	cgtcagcaag	gcggagaccg	gcgacaccgt	gagcttcgac	2820
ctggccgacg	atctggacgt	ctccgaaagc	atcacgggtg	gtgccgatcc	cgccgatccg	2880
aatgcgccga	ccactgttat	caccggcggt	tcgatcgtga	tcggcagcac	catgctcggc	2940
agcaacggcc	tggtcatcac	cggggggggcg	agcgtcacga	ccgatggcat	cgatgccggc	3000
ggcatgaagg	tcacgaatgt	ggcaaacgggt	acgggtggcg	aggattcgaa	ggatgccgtc	3060
aacggcgggc	agctcttcga	cgtcgttgcg	aatgccactg	cgaatggcgt	cggctatgac	3120
gacaaaagca	agggcaccct	gacgctggag	ggggctaacc	gcaccaagat	caccaatgtc	3180
gccgcggggcg	acctgaacgc	gaactcgacc	gacgcgggtca	acggcgagcca	gctttacgcc	3240
acgaacgtga	aggtcgatcg	gctcgatacc	gaagtgaag	agatcgacag	ccgcgtaacc	3300
tatatcgaga	gcttccaggg	cgatctggag	aacgctgccg	tctatgatac	cgacgctgcc	3360
ggcaagaggc	tcaaacacgt	gacgctcgag	ggaggagatc	ccgacaagcc	ggtgctcatc	3420
gccaatgtgg	ccaaggggcgt	gaaggcgacc	gacgccgtca	atgtcggcca	gctcgacgaa	3480
agcgtcgcg	aaagcaagag	ctacacggac	gaaaagaccg	agtgggcgat	cgatcaggcg	3540
gccatctaca	ccgaccagggt	tatcgagacc	aagggtgagcg	cgggtgaaca	ttatgcgcaa	3600
caacgggttcg	cgcagctctc	gggcgagatc	gggcagggttc	ggagcgaagc	gcggcaagcc	3660
gccgccatcg	gacttgcggc	ggcctcgctg	cgcttcgaca	atgagccggg	caagctgagc	3720
gtggcgctcg	gcggcggtt	ctggagaagc	gaaggggcg	tcgccttcgg	tgccggctac	3780
accagcgaag	acggacgcgt	ccgggcgaac	ctgaccgggtg	ctgcggccgg	ggggaacgtc	3840
ggtgtcggtg	ccggcctcag	catcacgctc	aactga			3876

<210> 36
 <211> 1119
 <212> DNA
 <213> *Bradorhizobium japonicum*

<400>	36					
gtgcggggcct	tcggctccgg	caacgccatc	aacggcacca	actacgcggc	cgtcgggtcc	60
aacaacgtcg	tcgccggcaa	caacggcgcg	gttgctcggt	ccggcaacgg	cgtcaccggc	120

gacaacaccg	cggccttcg	ctccagtatc	ggcatcgccg	gcggcaacaa	cgcggtgtgc	180
ggctccttca	gcaccgtcac	cggcagcaac	agcgcggctg	ttggctcctt	caacaacgtc	240
agcggcaata	acagcggcgc	ctttggcacc	ggacagaaca	tccgcggtaa	cggcacgttc	300
gccatcggcg	atcccaacat	cgtcaacggc	aacaacagtt	tgggtgttcg	cgacaacaac	360
acggtgaacg	ggtccaatgt	ggcgggtcgc	ggcgacaaca	tccagctggt	cggctcgaac	420
aacaccattg	cggcaacgtc	cagcgccgcc	ggctcatccg	tggtcggcag	cggcaacacc	480
gtcaacgcca	ccaatgccgt	ggtgatgggc	aacaacagca	ccgtctccgg	cgcgctcctt	540
gtcgcgatcg	gcaatggcac	ggccgttacc	ggcatcaacg	cgatcgcgat	gggcaccggc	600
gccggcgcga	atttcgacaa	ctcggtcgcg	atcggcagcg	gcgcgaccac	gacgcgcgcc	660
aaccaggtcg	cagtcggcac	cgccagcagc	acctacacga	tgagcggcat	cacctcggct	720
gcgagcaagg	cggcgcagtc	cggaccgacc	cagctcgtca	catcggacgc	ggccggcaat	780
ctggcgacca	cctcgctggc	tggcctcgga	cttgccctccg	ccggcgacat	caacggaatc	840
aactcccaac	tggccgccct	caacggccgc	gtcgacaacc	tgacacggga	gtcgcgcggc	900
ggcgtggcgt	tggcgctcgc	ggcgtccagc	ctgcaattcg	atcctcgccc	cggcaagatc	960
tcggtctccg	gcggcttcgg	caatttccag	ggacaatccg	gcctcgcggt	cggcctcggc	1020
tattcctatt	cggacgccat	gcgcttcaac	gcggcgttca	cggccgcaca	gcaaggcgcc	1080
atcggcgctca	gggccggcgc	gtcgtggacg	ctgaactga			1119

<210> 37
 <211> 364
 <212> PRT
 <213> Neisseria meningitidis

<400> 37
 Met Ser Met Lys His Phe Pro Ser Lys Val Leu Thr Thr Ala Ile Leu
 1 5 10 15
 Ala Thr Phe Cys Ser Gly Ala Leu Ala Ala Thr Ser Asp Asp Asp Val
 20 25 30
 Lys Lys Ala Ala Thr Val Ala Ile Val Ala Ala Tyr Asn Asn Gly Gln
 35 40 45
 Glu Ile Asn Gly Phe Lys Ala Gly Glu Thr Ile Tyr Asp Ile Gly Glu
 50 55 60
 Asp Gly Thr Ile Thr Gln Lys Asp Ala Thr Ala Ala Asp Val Glu Ala
 65 70 75 80
 Asp Asp Phe Lys Gly Leu Gly Leu Lys Lys Val Val Thr Asn Leu Thr
 85 90 95
 Lys Thr Val Asn Glu Asn Lys Gln Asn Val Asp Ala Lys Val Lys Ala
 100 105 110
 Ala Glu Ser Glu Ile Glu Lys Leu Thr Thr Lys Leu Ala Asp Thr Asp
 115 120 125
 Ala Ala Leu Ala Asp Thr Asp Ala Ala Leu Asp Glu Thr Thr Asn Ala
 130 135 140
 Leu Asn Lys Leu Gly Glu Asn Ile Thr Thr Phe Ala Glu Glu Thr Lys
 145 150 155 160
 Thr Asn Ile Val Lys Ile Asp Glu Lys Leu Glu Ala Val Ala Asp Thr
 165 170 175
 Val Asp Lys His Ala Glu Ala Phe Asn Asp Ile Ala Asp Ser Leu Asp
 180 185 190
 Glu Thr Asn Thr Lys Ala Asp Glu Ala Val Lys Thr Ala Asn Glu Ala
 195 200 205
 Lys Gln Thr Ala Glu Glu Thr Lys Gln Asn Val Asp Ala Lys Val Lys

145					150					155					160
Ser	His	Val	Ala	Ala	Asn	His	Gly	Tyr	Ser	Ile	Ala	Ile	Gly	Asp	Arg
				165					170					175	
Ser	Lys	Thr	Asp	Arg	Glu	Asn	Ser	Val	Ser	Ile	Gly	His	Glu	Ser	Leu
			180					185					190		
Asn	Arg	Gln	Leu	Thr	His	Leu	Ala	Ala	Gly	Thr	Lys	Asp	Thr	Asp	Ala
		195					200					205			
Val	Asn	Val	Ala	Gln	Leu	Lys	Lys	Glu	Ile	Glu	Lys	Thr	Gln	Glu	Asn
	210					215					220				
Thr	Asn	Lys	Arg	Ser	Ala	Glu	Leu	Leu	Ala	Asn	Ala	Asn	Ala	Tyr	Ala
225					230					235					240
Asp	Asn	Lys	Ser	Ser	Ser	Val	Leu	Gly	Ile	Ala	Asn	Asn	Tyr	Thr	Asp
				245					250					255	
Ser	Lys	Ser	Ala	Glu	Thr	Leu	Glu	Asn	Ala	Arg	Lys	Glu	Ala	Phe	Ala
			260					265					270		
Gln	Ser	Lys	Asp	Val	Leu	Asn	Met	Ala	Lys	Ala	His	Ser	Asn	Ser	Val
		275					280					285			
Ala	Arg	Thr	Thr	Leu	Glu	Thr	Ala	Glu	Glu	His	Ala	Asn	Ser	Val	Ala
	290					295					300				
Arg	Thr	Thr	Leu	Glu	Thr	Ala	Glu	Glu	His	Ala	Asn	Lys	Lys	Ser	Ala
305					310					315					320
Glu	Ala	Leu	Ala	Ser	Ala	Asn	Val	Tyr	Ala	Asp	Ser	Lys	Ser	Ser	His
				325					330					335	
Thr	Leu	Lys	Thr	Ala	Asn	Ser	Tyr	Thr	Asp	Val	Thr	Val	Ser	Asn	Ser
			340					345					350		
Thr	Lys	Lys	Ala	Ile	Arg	Glu	Ser	Asn	Gln	Tyr	Thr	Asp	His	Lys	Phe
		355					360					365			
Arg	Gln	Leu	Asp	Asn	Arg	Leu	Asp	Lys	Leu	Asp	Thr	Arg	Val	Asp	Lys
	370					375					380				
Gly	Leu	Ala	Ser	Ser	Ala	Ala	Leu	Asn	Ser	Leu	Phe	Gln	Pro	Tyr	Gly
385					390					395					400
Val	Gly	Lys	Val	Asn	Phe	Thr	Ala	Gly	Val	Gly	Gly	Tyr	Arg	Ser	Ser
				405					410					415	
Gln	Ala	Leu	Ala	Ile	Gly	Ser	Gly	Tyr	Arg	Val	Asn	Glu	Asn	Val	Ala
			420					425					430		
Leu	Lys	Ala	Gly	Val	Ala	Tyr	Ala	Gly	Ser	Ser	Asp	Val	Met	Tyr	Asn
		435					440					445			
Ala	Ser	Phe	Asn	Ile	Glu	Trp									
450					455										

<210> 39
 <211> 491
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Consensus of NadA family sequences

<220>

<221> Xaa

<222> 2, 3, 6, 7, 9, 10, 14, 17, 19, 23, 28, 30, 32, 33, 34, 40, 41, 43, 45, 47, 49, 50, 51, 53-66, 69, 71-75, 78, 84, 90-95, 99, 101-105, 117-119, 123, 126, 127, 129-131, 137, 146, 151-155, 157, 158, 160, 161, 164, 166, 210, 212-214, 216, 218, 222, 223, 231, 233, 236, 237, 239, 240, 243, 244, 246, 247, 249, 250-253, 256-260, 262-264, 266, 267, 271-284, 286, 288, 290, 296, 298, 300, 303, 305, 308-325, 333, 334, 336, 338-340, 342-344, 348, 349, 352, 354, 355, 360, 362, 363, 366-369, 371, 372, 374, 375, 377, 382, 384, 388, 391, 393, 394, 401, 409, 413, 445, 447, 448, 450, 454, 457, 463, 471, 475, 483

<223> Xaa is any amino acid

<400> 39

Met Xaa Xaa Met Lys Xaa Xaa Lys Xaa Xaa Leu Leu Ala Xaa Ala Ile
1 5 10 15

Xaa Ala Xaa Phe Ser Xaa Gly Ala Leu Ala Ala Xaa Thr Xaa Asp Xaa
20 25 30

Xaa Xaa Thr Gly Pro Glu Ala Xaa Xaa Val Xaa Ile Xaa Pro Xaa Ala
35 40 45

Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
50 55 60

Xaa Xaa Gly Leu Xaa Ala Xaa Ala Xaa Xaa Xaa Xaa Ser Ser Xaa Ala
65 70 75 80

Asp Ala Glu Ala Xaa Val Phe Lys Gly Leu Xaa Xaa Xaa Xaa Xaa Xaa
85 90 95

Pro Asn Ile Xaa Thr Xaa Xaa Xaa Xaa Xaa Gln Thr Lys Asp Gln Ile
100 105 110

Ala Met Leu Ile Arg Xaa Xaa Xaa Asn Leu Xaa Glu Asn Lys Xaa Xaa
115 120 125

Val Xaa Xaa Xaa Val Ala Ala Ile Lys Xaa Ile Pro Lys Asp Leu Ile
130 135 140

Ala Lys Xaa Ala Asp Val Asp Xaa Xaa Xaa Xaa Xaa Val Xaa Xaa Ala
145 150 155 160

Xaa Xaa Arg Xaa Thr Xaa Ala Xaa Asn Asn Leu Lys Ser Gly His Ser
165 170 175

Ser His Val Ala Ala Asn His Gly Tyr Ser Ile Ala Ile Gly Asp Arg
180 185 190

Ser Lys Thr Asp Arg Glu Asn Ser Val Ser Ile Gly His Glu Ser Leu
195 200 205

Asn Arg Xaa Leu Xaa Xaa Xaa Ala Xaa Lys Xaa Lys Glu Glu Xaa Xaa
210 215 220

Glu Asn Ile Ala Gln Ile Asp Xaa Asn Xaa Glu Gln Xaa Xaa Glu Xaa
225 230 235 240

Xaa Asp Lys Xaa Xaa Glu Xaa Xaa Asn Xaa Xaa Xaa Xaa Xaa Leu Ala
245 250 255

Xaa Xaa Xaa Xaa Xaa Ala Xaa Xaa Xaa Ala Xaa Xaa Val Asn Leu Xaa
 260 265 270
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr Thr Xaa Asn
 275 280 285
 Xaa Leu Xaa Gln Lys Ile Ala Glu Xaa Lys Xaa Asn Xaa Asp Ala Xaa
 290 295 300
 Lys Xaa Lys Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 305 310 315 320
 Xaa Xaa Xaa Xaa Xaa Xaa Ala Xaa Asn Thr Lys Asp Ile Xaa Xaa Leu
 325 330 335
 Xaa Thr Xaa Xaa Xaa Asp Xaa Xaa Xaa Asn Ser Ala Xaa Xaa Ala Ala
 340 345 350
 Xaa Thr Xaa Xaa Ile Ala Thr Glu Xaa Ser Xaa Xaa Phe Glu Xaa Xaa
 355 360 365
 Xaa Xaa Lys Xaa Xaa Gln Xaa Xaa Gln Xaa Ile Ala Asn Asn Xaa Thr
 370 375 380
 Xaa Val Ala Ile Xaa Glu Gln Xaa Ile Xaa Xaa Asn Thr Ala Arg Ile
 385 390 395 400
 Asp Xaa Leu Asp Asn Arg Val Asn Xaa Leu Asp Lys Glu Xaa Lys Ala
 405 410 415
 Gly Leu Ala Ser Gln Ala Ala Leu Ser Gly Leu Phe Gln Pro Tyr Asn
 420 425 430
 Val Gly Lys Leu Asn Val Ser Ala Ala Val Gly Gly Tyr Xaa Ser Xaa
 435 440 445
 Xaa Ala Xaa Ala Ile Gly Xaa Gly Ser Xaa Arg Phe Asn Glu Asn Xaa
 450 455 460
 Ala Ala Lys Ala Gly Val Ala Xaa Asp Thr Gln Xaa Gly Gly Ser Ser
 465 470 475 480
 Ala Gly Tyr Xaa Val Gly Val Asn Phe Glu Trp
 485 490

<210> 40
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> forward oligonucleotide primer HOM F

<400> 40
 tatcggcaaa cgacgcaagc 20

<210> 41
 <211> 20
 <212> DNA
 <213> reverse oligonucleotide primer HOM R2

<400> 41
 gggcgattag ccattgatac 20

<210>	42	
<211>	20	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	reverse oligonucleotide primer HOM R3	
<400>	42	20
	aacggttgat gccgcactag	
<210>	43	
<211>	22	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	forward primer for HadA locus	
<400>	43	22
	gtgttgatag gtggcactac tg	
<210>	44	
<211>	23	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	forward primer for HadA locus	
<400>	44	23
	gcagagaaag caaaaggtga ttc	
<210>	45	
<211>	23	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	forward primer for HadA locus	
<400>	45	23
	caaaattctg cagacatcgc aac	
<210>	46	
<211>	20	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	forward primer for HadA locus	
<400>	46	20
	caaactgcag ttgctgtagg	
<210>	47	
<211>	21	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	reverse primer for HadA locus	

```

<400> 47
acctacagca actgcagttt g 21

<210> 48
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> reverse primer for HadA locus

<400> 48
caactccctc ttctaaagct g 21

<210> 49
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> reverse primer for HadA locus

<400> 49
agtagtgcca cctatcaaca c 21

<210> 50
<211> 1339
<212> DNA
<213> Haemophilus sp

<400> 50
cgacgcaagc caagtaatag taatatttaa ttaggtatga tgtaaattct gcttgaggca 60
aattttacat aggaaatttt tctatattgc tttaacgttt ttttatagta gaagtatata 120
ctcagttatg gttatgggta catagtatag ttttactttg ttctagttca ctttaataac 180
cttaaataat tgaggatttc ttatgaaaag aaattttatta aaacaatctg taatcgctgt 240
gttgataggt ggcactactg tttctaatta tgcttttagca caagcacaag cacaagcaca 300
agtcaaaaaa gatgaactta gtgagttaaa gaaacaagta aaggaaatgg atgctgctat 360
cgatgggtatt cttgatgata atatttgctta tgaagctgaa gttgatgcaa aacttgatca 420
gcattctgct gctcttggtg gacatacaaa tagactcaat aatcttaaaa cgattgcaga 480
gaaagcaaaa ggtgattcaa gtgaagcact tgataaaatt gaagctcttg aagaacaaaa 540
tgatgagttt ttagcggata ttacagcttt agaagaggga gttgatgggt tagatgatga 600
tatcacaggt attcaagata atatttctga tatagaagat gatattaatc aaaattctgc 660
agacattgca actaacacag cggcaatcgc aactcacact caacgtcttg ataatttaga 720
taacagagta aataacctta ataaagatct taaacgtggg cttgctgctc aagctgcatt 780
aaatgggttta ttccaaccgt ataacgtagg taaattaaat cttactgctg ctgtaggtgg 840
ttataaatct caaactgcag ttgctgtagg tactgggttat cgttataacg aaaatatcgc 900
ggctaaagca ggtggtgctt tcactcatgg tggcagcgca acttataatg ttggcgtaaa 960
ttttgaatgg taattagata actaattttc cataacagaa aataaatacc tgtttttgag 1020
taatatcaga aacaggtatt tttttatagg cttcgtttcg cacactcgtt actagtgtgg 1080
atatgtgaat aaaatcaata atatttggag tatttcatct attttattaa ttttgttagc 1140
ggataaaata acttttctgtg tgttcctcca aattctttta attcaataaa ccctaatacgt 1200
tcataaaacg agctggcatc atcatttttt gcttcaacga ctaaaattgt agcagctacc 1260
gtagcattct taatcttatg aatggcgtct gcaattagaa actttccata cccttgcttc 1320
tggaattcgt tatcaatgg 1339

<210> 51
<211> 256
<212> PRT
<213> Haemophilus sp

<400> 51
Met Lys Arg Asn Leu Leu Lys Gln Ser Val Ile Ala Val Leu Ile Gly
1 5 10 15

```

Gly Thr Thr Val Ser Asn Tyr Ala Leu Ala Gln Ala Gln Ala Gln Ala
 20 25 30
 Gln Val Lys Lys Asp Glu Leu Ser Glu Leu Lys Lys Gln Val Lys Glu
 35 40 45
 Met Asp Ala Ala Ile Asp Gly Ile Leu Asp Asp Asn Ile Ala Tyr Glu
 50 55 60
 Ala Glu Val Asp Ala Lys Leu Asp Gln His Ser Ala Ala Leu Gly Arg
 65 70 75 80
 His Thr Asn Arg Leu Asn Asn Leu Lys Thr Ile Ala Glu Lys Ala Lys
 85 90 95
 Gly Asp Ser Ser Glu Ala Leu Asp Lys Ile Glu Ala Leu Glu Glu Gln
 100 105 110
 Asn Asp Glu Phe Leu Ala Asp Ile Thr Ala Leu Glu Glu Gly Val Asp
 115 120 125
 Gly Leu Asp Asp Asp Ile Thr Gly Ile Gln Asp Asn Ile Ser Asp Ile
 130 135 140
 Glu Asp Asp Ile Asn Gln Asn Ser Ala Asp Ile Ala Thr Asn Thr Ala
 145 150 155 160
 Ala Ile Ala Thr His Thr Gln Arg Leu Asp Asn Leu Asp Asn Arg Val
 165 170 175
 Asn Asn Leu Asn Lys Asp Leu Lys Arg Gly Leu Ala Ala Gln Ala Ala
 180 185 190
 Leu Asn Gly Leu Phe Gln Pro Tyr Asn Val Gly Lys Leu Asn Leu Thr
 195 200 205
 Ala Ala Val Gly Gly Tyr Lys Ser Gln Thr Ala Val Ala Val Gly Thr
 210 215 220
 Gly Tyr Arg Tyr Asn Glu Asn Ile Ala Ala Lys Ala Gly Val Ala Phe
 225 230 235 240
 Thr His Gly Gly Ser Ala Thr Tyr Asn Val Gly Val Asn Phe Glu Trp
 245 250 255

<210> 52
 <211> 33
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HadA C-terminus

<400> 52
 Thr Gly Tyr Arg Tyr Asn Glu Asn Ile Ala Ala Lys Ala Gly Val Ala
 1 5 10 15
 Phe Thr His Gly Gly Ser Ala Thr Tyr Asn Val Gly Val Asn Phe Glu
 20 25 30

Trp

<210> 53
 <211> 519
 <212> DNA
 <213> Haemophilus sp

<400> 53
 atgataaatg aaaatttagc atattttaagt gtattaccct tagaagatgt aaagattgag 60
 agaagttcat tttcttggtc agttgaacct ttagaaaact actttcataa gtacgtttct 120
 caagatgtaa agaaagggct tgcaaagtgt tttgtgctta taaatgcaca accatctagg 180
 attgttggct attacacttt atcggcatta tcaataccaa ttccagatat accccaagaa 240
 cgaataagta aaggcgtacc atatcctaatt attcctgctg ttttaatagg gcgattagcc 300
 attgatacga atttccagaa gcaaggggat ggaaagtttc taattgcaga cgccattcat 360
 aagattaaga atgctacggt agctgctaca atttttagtcg ttgaagcaaa aaatgatgat 420
 gccagctcgt tttatgaacg attaggggtt attgaattta aagaatttgg aggaacacac 480
 agaaagttat tttatccgct aacaaaatta ataaaatag 519

<210> 54
 <211> 172
 <212> PRT
 <213> Haemophilus sp

<400> 54
 Met Ile Asn Glu Asn Leu Ala Tyr Leu Ser Val Leu Pro Leu Glu Asp
 1 5 10 15
 Val Lys Ile Glu Arg Ser Ser Phe Ser Cys Ser Val Glu Pro Leu Glu
 20 25 30
 Asn Tyr Phe His Lys Tyr Val Ser Gln Asp Val Lys Lys Gly Leu Ala
 35 40 45
 Lys Cys Phe Val Leu Ile Asn Ala Gln Pro Ser Arg Ile Val Gly Tyr
 50 55 60
 Tyr Thr Leu Ser Ala Leu Ser Ile Pro Ile Pro Asp Ile Pro Gln Glu
 65 70 75 80
 Arg Ile Ser Lys Gly Val Pro Tyr Pro Asn Ile Pro Ala Val Leu Ile
 85 90 95
 Gly Arg Leu Ala Ile Asp Thr Asn Phe Gln Lys Gln Gly Tyr Gly Lys
 100 105 110
 Phe Leu Ile Ala Asp Ala Ile His Lys Ile Lys Asn Ala Thr Val Ala
 115 120 125
 Ala Thr Ile Leu Val Val Glu Ala Lys Asn Asp Asp Ala Ser Ser Phe
 130 135 140
 Tyr Glu Arg Leu Gly Phe Ile Glu Phe Lys Glu Phe Gly Gly Thr His
 145 150 155 160
 Arg Lys Leu Phe Tyr Pro Leu Thr Lys Leu Ile Lys
 165 170

<210> 55
 <211> 168
 <212> PRT
 <213> Haemophilus somnus

<400> 55
 Met Ile Asn Glu Asn Leu Ala Tyr Leu Ser Val Leu Pro Leu Glu Asp
 1 5 10 15

Val Lys Ile Glu Arg Ser Ser Phe Ser Cys Ser Val Glu Pro Leu Glu
 20 25 30
 Asn Tyr Phe His Lys Tyr Val Ser Gln Asp Val Lys Lys Gly Leu Ala
 35 40 45
 Lys Cys Phe Val Leu Ile Asn Ala Gln Pro Ser Arg Ile Val Gly Tyr
 50 55 60
 Tyr Thr Leu Ser Ala Leu Ser Ile Pro Ile Pro Asp Ile Pro Gln Glu
 65 70 75 80
 Arg Ile Ser Lys Gly Val Pro Tyr Pro Asn Ile Pro Ala Val Leu Ile
 85 90 95
 Gly Arg Leu Ala Ile Asp Thr Asn Phe Gln Lys Gln Gly Tyr Gly Lys
 100 105 110
 Phe Leu Ile Ala Asp Ala Ile His Lys Ile Lys Asn Ala Thr Val Ala
 115 120 125
 Ala Thr Ile Leu Val Val Glu Ala Lys Asn Asp Asp Ala Ser Ser Phe
 130 135 140
 Tyr Glu Arg Leu Gly Phe Ile Glu Phe Lys Glu Phe Gly Gly Thr His
 145 150 155 160
 Arg Lys Leu Phe Tyr Pro Leu Thr
 165

<210> 56
 <211> 172
 <212> DNA
 <213> Haemophilus influenzae strain 86028

<400> 56
 gcaagccaag taacagtaat gtttaattag gtatgattta aattctgttt tatatcacac 60
 tagcaatgtg ggtttcttgt attggtatta actaaattac gcattaataa agcgtaattt 120
 aagttaatat cttgtggtac atttaagaat acaaaatgcc catcacctag tg 172

<210> 57
 <211> 172
 <212> DNA
 <213> Haemophilus influenzae strain R2846

<400> 57
 gcaagccaag taacagtaat gtttaattag gtatgattta aattctgttt tatatcacac 60
 tagcaatgtg ggtttcttgt attggtatta actaaattac gcattaataa agcgtaattt 120
 aagttaatat cttgtggtac atttaagaat acaaaatgcc catcacctag tg 172

<210> 58
 <211> 172
 <212> DNA
 <213> Haemophilus influenzae strain NT36

<400> 58
 gcaagccaag taacagtaat gtttaattag gtatgattta aattctgttt tatatcacac 60
 tagcaatgtg ggtttcttgt attggtatta actaaattac gcattaataa agcgtaattt 120
 aagttaatat cttgtggtac atttaagaat acaaaatgcc catcgccctag tg 172

<210> 59
 <211> 172
 <212> DNA

<213> Haemophilus influenzae strain EAGAN

<400> 59

gcaagccaag	taacagtaat	gtttaattag	gtatgattta	aattctgttt	tatatcacac	60
tagcaatgcg	ggtttcttgt	attgggtatta	actaaattac	gcattaataa	agcgtaattt	120
aagttaatat	cttgtggtac	atttaagaat	acaaaatgcc	catcgcctag	tg	172

<210> 60

<211> 172

<212> DNA

<213> Haemophilus influenzae strain HK707

<400> 60

gcaagccaag	taacagtaat	gtttaattag	gtatgattta	aattctgttt	tatatcacac	60
tagcaatgcg	ggtttcttgt	attgggtatta	actaaattac	gcattaataa	agcgtaattt	120
aagttaatat	cttgtggtac	atttaagaat	acaaaatgcc	catcgcctag	tg	172

<210> 61

<211> 172

<212> DNA

<213> Haemophilus influenzae strain R2866

<400> 61

gcaagccaag	taacagtaat	gtttaattag	gtatgattta	aattctgttt	tatatcacac	60
tagaaatgag	gatttcttgt	attgggtatta	actaaattac	gcattaataa	ggcgtaattt	120
aagttaatat	cttgtggcac	atttaagaat	acaaaatgcc	catcgcctag	tg	172

<210> 62

<211> 21

<212> DNA

<213> Haemophilus influenzae

<400> 62

ttaggatatga	tttaaattct	g	21
-------------	------------	---	----

<210> 63

<211> 77

<212> DNA

<213> Haemophilus influenzae

<400> 63

atagtatatgt	tttactttgt	tctagttcac	tttaataacc	ttaaataatt	gaggatttct	60
tatgaaaaga	aatttat					77

<210> 64

<211> 300

<212> DNA

<213> Haemophilus influenzae

<400> 64

ccgacgcaag	ccaagtaata	gtaatattta	attaggtatg	atgtaaattc	tgcttgaggc	60
aaattttaca	taggaaattt	ttctatatgt	ctttaacgtt	tttttatagt	agaagtatat	120
actcagttat	ggttatgggt	acatagtata	gttttacttt	gttctagttc	actttaataa	180
ccttaaataa	ttgaggattt	cttatgaaaa	gaaattttatt	aaaacaatct	gtaatcgctg	240
tgttgatagg	tggcactact	gtttctaatt	atgcttttagc	acaagcacia	gcacaagcac	300

<210> 65

<211> 180

<212> DNA

<213> Haemophilus influenzae strain Rd and strain F1947

<400> 65

aggatacgaa	aaatatcggc	aaacgacgca	agccaagtaa	cagtaatggt	taggcttgta	60
tagtatagct	ttgctttgtt	ctagttcaat	ttaataatct	taaataatta	aggatttctt	120

atgaaaaaaaa atttataggc ttcgtttcgc acactcgttg ctagtataga tatgtgaata 180